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OM protein - protein search, using sw model

Run on: April 23, 2004, 16:21:29 / Search time 57 seconds
(without alignments)
738.589 Million cell updates/sec

Title: US-09-931-325c-170_COPY_1_149
Perfect score: 793
Sequence: 1 MDIDYKFGATVLLSLP.....PAYRPPNAPILSLPETTVV 149

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: A_Geneseq_29Jan04: *
1: Geneseq1980s: *
2: Geneseq1990s: *
3: Geneseq2000s: *
4: Geneseq2001s: *
5: Geneseq2002s: *
6: Geneseq2003as: *
7: Geneseq2003bs: *
8: Geneseq2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	793	100.0	171	5	AAU93972	Immunogen
2	793	100.0	183	2	AAV29674	Human hep
3	793	100.0	183	5	AAU87786	Human hep
4	793	100.0	183	5	AAU80906	Hepatitis
5	793	100.0	183	5	ABG94182	Hepatitis
6	793	100.0	183	5	AAU93961	Hepatitis
7	793	100.0	183	5	ABG80494	Hepatitis
8	793	100.0	183	6	ABO01919	Hepatitis
9	793	100.0	183	6	ABR56458	Hepatitis
10	793	100.0	183	6	ABR44571	Hepatitis
11	793	100.0	183	7	ADD24146	Hepatitis
12	793	100.0	183	7	ADE10767	Hepatitis
13	793	100.0	183	7	AAW50242	Human Hep
14	793	100.0	212	2	AAW50250	Hepatitis
15	793	100.0	212	5	AAU80921	Hepatitis
16	793	100.0	212	5	ABG34187	Hepatitis
17	793	100.0	212	5	AAE19898	Hepatitis
18	793	100.0	212	5	AAE19793	Hepatitis
19	793	100.0	212	5	ABG80509	Hepatitis
20	793	100.0	212	5	ABR56483	Hepatitis
21	793	100.0	212	6	ABR56483	Hepatitis
22	793	100.0	212	6	ABR44586	Hepatitis
23	793	100.0	212	7	ABW00349	Hepatitis
24	793	100.0	212	7	ADD24161	Hepatitis
25	793	100.0	289	2	AAW09049	Plasmid p

26	793	100.0	346	2	AAU27473	SI2/core
27	793	100.0	397	2	AAW09048	Plasmid p
28	791	99.7	183	5	AAU80909	Hepatitis
29	791	99.7	183	5	ABG94185	Hepatitis
30	791	99.7	183	5	ABG80497	Hepatitis
31	791	99.7	183	5	ABR56471	Synthetic
32	791	99.7	183	6	ABR56471	Synthetic
33	791	99.7	183	7	ADD24149	Hepatitis
34	790	99.6	183	5	AAU80911	Hepatitis
35	790	99.6	183	5	AAU80912	Hepatitis
36	790	99.6	183	5	ABG94187	Hepatitis
37	790	99.6	183	5	ABG94188	Hepatitis
38	790	99.6	183	5	ABG80500	Hepatitis
39	790	99.6	183	5	ABG80499	Hepatitis
40	790	99.6	183	6	ABR56474	Hepatitis
41	790	99.6	183	6	ABR44576	Hepatitis
42	790	99.6	183	6	ABR44577	Hepatitis
43	790	99.6	183	6	ABR44577	Hepatitis
44	790	99.6	183	7	ADD24151	Hepatitis
45	790	99.6	183	7	ADD24152	Hepatitis

ALIGNMENTS

RESULT 1

AAU93972
ID AAU93972 standard; peptide; 171 AA.
XX
AC AAU93972;
XX
DT 02-JUL-2002 (first entry)
XX
DE Immunogenic HBC chimeric particle #9.
XX
KW Immunogenic; hepatitis B core protein; immunostimulant.
KW vaccine; B cell epitope; T cell epitope; immunostimulant.
XX
OS Plasmodium falciparum.
XX
PN WO200214478-A2.
XX
PD 21-FEB-2002.
XX
PF 16-AUG-2001; 2001WO-US041759.
XX
PR 16-AUG-2000; 2000US-0225843P.
PR 22-AUG-2000; 2000US-0226867P.
PR 15-AUG-2001; 2001US-00930915.
XX
XX (APOV-) APOVIA INC.
XX
XX Birkett AJ;
XX
XX WPI; 2002-257601/30.
XX
XX Novel recombinant hepatitis B core protein, termed as chimeric hepatitis B core protein, displays immunogenic epitopes at N-terminus, HBC immunogenic loop with linker for conjugated epitope and C-terminus.
XX
XX Example 4; Page 273; 289pp; English.

The invention relates to a recombinant hepatitis B core protein, displaying one or i.e. a chimeric hepatitis B core (HBC) protein (I), displaying one or more immunogenic epitopes at the N-terminus, HBC immunogenic loop (L) or C-terminus, or having a heterologous linker for a conjugated epitope in (L), and containing a Cys residue at, or near, the C-terminus that confers enhanced stability to the particles. A vaccine comprising (I) is useful for inducing an immune response in an inoculated host animal, by inoculating a host animal with the vaccine, and maintaining that animal for a time period sufficient for that animal to develop an immune response. The immunogenic particles formed using (I) are substantially free of binding to nucleic acids, and are most stable than

CC the particle formed from otherwise identical HBC chimera that lacks the C-
CC terminal residue or in which a C-terminal Cys is replaced by another
CC residue. The chimera particles are most stable on storage in aqueous
CC compositions that are particles of similar sequence that lack any C-
CC terminal Cys residues. The chimera molecule exhibits the self-assembly not
CC exhibiting the nucleic acid binding of those native particles, and
CC excellent B cell and T cell immunogenicities. The chimera particles are
CC typically prepared in higher yield than similar particles that are free
CC of a C-terminal Cys. The particles are often far more immunogenic than
CC the similar conjugates that lack a C-terminal Cys. Immunogenicities of
CC particles assembled from the chimera molecules are enhanced as compared to
CC similar particles assembled from chimera molecules lacking at least one C-
CC terminal Cys. AAU93802-AAU93997 represent immunogenic HBC particles amino
CC acid sequences and related sequences of the invention
XX
SQ Sequence 171 AA;

Query Match 100.0%; Score 793; DB 5; Length 171;
Best Local Similarity 100.0%; Pred. NO. 8.8e-85;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDIDPYKEFGATVELLSFLPSDFPSVDRDLDTASALYREALSPHCSPHHTALRQAIL 60
DB 1 MDIDPYKEFGATVELLSFLPSDFPSVDRDLDTASALYREALSPHCSPHHTALRQAIL 60
QY 61 CWGELMTLATWGVNLEDPASRDVSVYNTNMGKPKQLLWTHISCLTFRGTVEIYLV 120
DB 61 CWGELMTLATWGVNLEDPASRDVSVYNTNMGKPKQLLWTHISCLTFRGTVEIYLV 120
QY 121 SFGWIRTPPAYRPPNAPILSTLPETTV 149
DB 121 SFGWIRTPPAYRPPNAPILSTLPETTV 149

RESULT 2
AAU29674
ID AAU29674 standard; protein; 183 AA.
XX
AC AAU29674;
XX
DT 08-NOV-1999 (first entry)
XX
DE Human hepatitis B core protein.
XX
KW Human hepatitis B core protein; HBC; modified; immunodominant;
KW nucleocapsid protein; vaccine; T cell epitope.
XX
OS Hepatitis B virus.
XX
PN WO9940934-A1.
XX
PD 19-AUG-1999.
XX
PF 11-FEB-1999; 99WO-US003055.
XX
PR 12-FEB-1998; 98US-0074537P.
XX
PA (IMMU-) IMMUNE COMPLEX CORP.
XX
PI Birkett AJ;
XX
PI WPI; 1999-527340/44.
XX
DR N-PSDB; AAZ08316.
XX

Conjugate of hepatitis B core protein, modified to increase reactivity
PT with haptens, used to raise antibodies against the haptens, e.g. in
PT vaccines.
XX
PS Claim 17; Page 77-78; 128pp; English.
XX

The present invention describes a conjugate (A) comprising a
CC strategically modified hepatitis B core (HBC) protein (I) attached to a
CC haptens, where (I) includes amino acids (aa) 10-140 of the wild type HBC

CC 183 aa sequence (given in AAU29674) and additionally has an insert (II)
CC in the region corresponding to aa's 50-100, where the insert is of 1 to
CC about 40 aa's and containing a chemically reactive aa residue linked to the
CC haptens. A vaccine containing (A), optionally in the form of particles, is
CC used to induce a protective antibody response against the pathogen from
CC which the haptens is derived, in humans or other animals. These pathogens
CC may be bacteria, viruses, rickettsia or protozoa. Insertion of (II)
CC overcomes the low reactivity of aa side chains in native HBC protein,
CC increasing the reactivity with haptens and resulting in conjugates of
CC improved immunogenicity. Modified HBC can be derivatised in the form of
CC particles by well-defined chemical methods, and is unlikely to cause
CC immunological side-effects. The present sequence represents the wild type
CC HBC protein
XX
SQ Sequence 183 AA;

Query Match 100.0%; Score 793; DB 2; Length 183;
Best Local Similarity 100.0%; Pred. NO. 9.7e-85;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDIDPYKEFGATVELLSFLPSDFPSVDRDLDTASALYREALSPHCSPHHTALRQAIL 60
DB 1 MDIDPYKEFGATVELLSFLPSDFPSVDRDLDTASALYREALSPHCSPHHTALRQAIL 60
QY 61 CWGELMTLATWGVNLEDPASRDVSVYNTNMGKPKQLLWTHISCLTFRGTVEIYLV 120
DB 61 CWGELMTLATWGVNLEDPASRDVSVYNTNMGKPKQLLWTHISCLTFRGTVEIYLV 120
QY 121 SFGWIRTPPAYRPPNAPILSTLPETTV 149
DB 121 SFGWIRTPPAYRPPNAPILSTLPETTV 149

RESULT 3
AAU87796
ID AAU87796 standard; protein; 183 AA.
XX
AC AAU87796;
XX
DT 21-MAY-2002 (first entry)
XX
DE Human hepatitis B virus nucleocapsid protein #1.
XX
KW Hepatitis B virus; nucleocapsid protein; HBC; hepatitis B virus core;
KW B cell epitope; T cell epitope; malaria; HIV-1; Plasmodium; protozoacide;
KW circumsporozoite; human immunodeficiency virus type I; human; squirrel;
KW woodchuck.
XX
OS Homo sapiens.
XX
PN WO200213765-A2.
XX
PD 21-FEB-2002.
XX
PF 16-AUG-2001; 2001WO-US025625.
XX
PR 16-AUG-2000; 2000US-0225813P.
XX
PR 15-AUG-2001; 2001US-00931325.
XX
PA (APOV-) APOVIA INC.
XX
PI Birkett AJ;
XX
PI WPI; 2002-241832/29.
XX
DR N-PSDB; ABK44278.
XX

Recombinant hepatitis B virus core protein chimera molecule, useful to
PT induce antibodies to malarial parasites, comprises malaria-specific T-
PT cell epitope and is engineered for enhanced stability.
XX
PS Disclosure; Fig 6; 197pp; English.
XX
XX The invention relates to a recombinant hepatitis B virus core (HBC)

CC protein chimera molecule that contains 4 peptide-linked amino acid residue
 CC sequence domains. The molecule of the invention contains a region
 CC constituting a B cell epitope of the circumsporozoite protein of a
 CC species of the parasite, Plasmodium. The chimera sequence is useful as an
 CC immunogen for inducing antibodies to the malaria-causing parasite.
 CC Plasmodium, particularly P. falciparum and P. vivax. Sequences AAU87695-
 XX AAU87804 represent peptide epitopes of the invention
 XX
 CC Sequence 183 AA;

Query Match 100.0%; Score 793; DB 5; Length 183;
 Best Local Similarity 100.0%; Pred. No. 9.7e-85;
 Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDIDPYKEFGATVELLSFLPSDFPSVRLDLDTSALYREALSPHCSPHTALRQAIL 60
 DB 1 MDIDPYKEFGATVELLSFLPSDFPSVRLDLDTSALYREALSPHCSPHTALRQAIL 60
 QY 61 CWGELMTLATWGVNLEDPASRDLYVSYNTNMGKFRQLLWPHISCLTFGRETIVIELV 120
 DB 61 CWGELMTLATWGVNLEDPASRDLYVSYNTNMGKFRQLLWPHISCLTFGRETIVIELV 120
 QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVV 149
 DB 121 SFGVWIRTPPAYRPPNAPILSTLPETTVV 149

RESULT 4
 ID AAU80906 standard; protein; 183 AA.
 AC AAU80906;
 XX
 DT 09-APR-2002 (first entry)
 XX
 DE Hepatitis B virus core antigen variant (HBCAg) #11.
 DE
 KW Vaccine; molecular scaffold; pilus; pilin; HBCAg; antigen;
 KW hepatitis B virus capsid protein; JUN; FOS; HIV gp140;
 KW measles virus N protein; bee venom phospholipase; Th type 2 T-helper;
 KW Th2; Sinbis virus E2 protein; amyloid beta; influenza M2 antigen;
 KW human immunodeficiency virus infection; viral hepatitis; measles;
 KW chicken pox; pneumonia; tuberculosis; syphilis; malaria; allergy; cancer;
 KW chronic disease; arthritis; colitis; diabetes; multiple sclerosis.
 XX
 OS Hepatitis B virus.
 XX
 XX WO200185208-A2.
 XX
 XX 15-NOV-2001.
 XX
 XX 02-MAY-2001; 2001WO-IB000741.
 XX
 XX 05-MAY-2000; 2000US-0202341P.
 XX
 XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
 XX
 XX (SEBEL P. SEBEL P.
 XX (DUNA/) DUNANT N.
 XX (BACH/) BACHMANN M.
 XX (TISS/) TISSOT A.
 XX (LECH/) LECHENER F.
 XX
 XX Sebel P, Dunant N, Bachmann M, Tissot A, Lechner F;
 PI
 XX WPI; 2002-055561/07.
 XX
 XX New composition, useful for vaccine production, comprises antigen or
 PT antigenic determinant and non-natural molecular scaffold comprising
 PT organizer and core particle such as bacterial pilus or pilin protein.
 XX
 PS Claim 34; Page 216-217; 287pp; English.
 PS
 XX The invention relates to a composition comprising: (a) a non-natural

CC molecular scaffold (molecular scaffold) which comprises a core particle
 CC such as a bacterial pilus or pilin protein, a recombinant form of the
 CC protein, a virus-like particle or a hepatitis B virus capsid protein
 CC (HBCAg), and an organizer; and (b) an antigen or antigenic determinant,
 CC where the molecular scaffold and antigenic determinant interact to form
 CC an ordered and repetitive antigen array. Suitable antigenic determinants
 CC include JUN, FOS, HIV gp140, measles virus N protein, bee venom
 CC phospholipase, Sinbis virus E2 protein, amyloid beta derived peptides and
 CC influenza M2 antigen. The composition (or vaccine) is useful for
 CC immunisation, by administration to a subject, where the administration
 CC produces an immune response, such as humoral, cellular or protective
 CC immune response, preferably a Th type 2 T-helper (Th2) response that is
 CC specific for the antigenic determinant. The administration induces
 CC antibodies specific for the antigenic determinant of a subtype
 CC corresponding to the Th2 subtype in the subject. The subject does not
 CC generate a Th2 subtype that is specific for pilus or pilin polypeptide or
 CC antigenic determinant. The composition is useful for the production of
 CC vaccines for prevention of infectious diseases such as human
 CC immunodeficiency virus, viral hepatitis, measles, chicken pox, pneumonia,
 CC tuberculosis, syphilis, malaria, and for treating allergy, cancer, and
 CC chronic diseases induced or accelerated by a Th1 type immune response,
 CC such as arthritis, colitis, diabetes and multiple sclerosis. The
 CC composition is useful to generate defined self-specific antibodies and
 CC specific immune responses of the Th2 type and allows the creation of
 CC highly efficient vaccines against infectious diseases, and for treating
 CC allergy, cancer, and chronic diseases induced or accelerated by a Th1
 CC type immune response. The present sequence is a peptide or protein
 CC incorporated into the compositions of the invention
 XX
 CC Sequence 183 AA;

Query Match 100.0%; Score 793; DB 5; Length 183;
 Best Local Similarity 100.0%; Pred. No. 9.7e-85;
 Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDIDPYKEFGATVELLSFLPSDFPSVRLDLDTSALYREALSPHCSPHTALRQAIL 60
 DB 1 MDIDPYKEFGATVELLSFLPSDFPSVRLDLDTSALYREALSPHCSPHTALRQAIL 60
 QY 61 CWGELMTLATWGVNLEDPASRDLYVSYNTNMGKFRQLLWPHISCLTFGRETIVIELV 120
 DB 61 CWGELMTLATWGVNLEDPASRDLYVSYNTNMGKFRQLLWPHISCLTFGRETIVIELV 120
 QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVV 149
 DB 121 SFGVWIRTPPAYRPPNAPILSTLPETTVV 149

RESULT 5
 ID ABG94182
 AC ABG94182 standard; protein; 183 AA.
 XX
 AC ABG94182;
 XX
 DT 10-DEC-2002 (first entry)
 XX
 DE Hepatitis B capsid (core) protein antigen (HBCAg) variant #11.
 XX
 XX Human; mouse; rat; antimicrobial; antiallergic; immunomodulatory;
 KW cytosolic; antiviral; antidiabetic; hypoglycaemic; antigen array;
 KW vaccine; infectious disease.
 XX
 OS Hepatitis B virus.
 XX
 XX WO200256905-A2.
 XX
 XX 25-JUL-2002.
 XX
 XX 21-JAN-2002; 2002WO-IB000166.
 PF
 XX 19-JAN-2001; 2001US-0262379P.
 PR 04-MAY-2001; 2001US-0288549P.
 PR 05-OCT-2001; 2001US-0326998P.

PR 07-NOV-2001; 2001US-0331045P.
XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX Renner WA, Bachmann M, Tissot A, Maurer P, Lechner F, Sebbel P;
PI Plossek C;
XX WPI; 2002-627351/67.
XX Molecular antigen array used in the production of vaccines for infectious
PT diseases.
XX Claim 112; Page 337-338; 441pp; English.
XX This invention relates to a novel ordered and repetitive antigen array
CC used in the production of vaccines for infectious diseases. The invention
CC also discloses a composition comprising a non-natural molecular scaffold
CC comprising a core particle selected from a core particle of a non-natural
CC origin and a core particle of natural origin and an organiser comprising
CC at least one first attachment site, where the organiser is connected to
CC the core particle by at least one covalent bond. Also disclosed is an
CC antigen or antigenic determinant with at least one second attachment
CC site, where the antigen or antigenic determinant is anyloid beta peptide
CC (Abeta1-42) or its fragment and where the second attachment site is
CC selected from an attachment site not naturally occurring with the antigen
CC or antigenic determinant and an attachment site naturally occurring with
CC the antigen or antigenic determinant, where the second attachment site is
CC capable of association through at least one non-peptide bond to the first
CC attachment site and where the antigen or antigenic determinant and the
CC scaffold interact through the association to form an ordered and
CC repetitive antigen array. The invention also comprises a coat protein
CC capable of forming a capsid which comprises mutant beta coat proteins
CC having an amino acid sequence selected from five amino acid sequences
CC fully defined in the specification. The compounds of the invention may
CC have antimicrobial, antiallergic, immunomodulatory, cytostatic,
CC antiviral, antidiabetic, or hypoglycaemic activities and may be used in
CC immunisation and as a vaccine. The present sequence represents a protein
CC sequence used to create the compositions of the invention
XX
SQ Sequence 183 AA;
Query Match 100.0%; Score 793; DB 5; Length 183;
Best Local Similarity 100.0%; Pred. No. 9.7e-85;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALQAIL 60
Db 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALQAIL 60
Qy 61 CWGELMTLATWGVNLEDPASRDVLVSVYNTNMGLKFRQLLWFHISCLTFGRETVEYLV 120
Db 61 CWGELMTLATWGVNLEDPASRDVLVSVYNTNMGLKFRQLLWFHISCLTFGRETVEYLV 120
Qy 121 SFGVWIRTPPAYRPPNAPILSTLPETTIV 149
Db 121 SFGVWIRTPPAYRPPNAPILSTLPETTIV 149
RESULT 6
AAU93961
ID AAU93961 standard; peptide; 183 AA.
XX AAU93961;
XX
XX 02-JUL-2002 (first entry)
XX Hepatitis B virus Hbc epitope #1.
XX Immunogenic; hepatitis B virus nucleocapsid protein; hepatitis B core; Hbc;
KW vaccine; B cell epitope; T cell epitope; immunostimulant.
XX
XX Hepatitis B virus.
OS
XX

PN WO200214478-A2.
XX
PD 21-FEB-2002.
XX
EP 16-AUG-2001; 2001WO-US041759.
XX
XX 12-AUG-2000; 2000US-0225843P.
PR 22-AUG-2000; 2000US-0226867P.
PR 15-AUG-2001; 2001US-00930915.
XX
XX (APOV-) APOVIA INC.
XX
XX Birkett AJ;
XX WPI; 2002-257601/30.
XX Novel recombinant hepatitis B core protein, displaying one or
PT hepatitis B core protein, displays immunogenic epitopes at N-terminus,
PT Hbc immunogenic loop with linker for conjugated epitope and C-terminus.
XX
PS Disclosure; Fig 7; 289pp; English.
XX The invention relates to a recombinant hepatitis B core protein, termed as chimeric
CC i.e. a chimeric hepatitis B core (Hbc) protein (I), displaying one or
CC more immunogenic epitopes at the N-terminus, Hbc immunogenic loop (L) or
CC C-terminus, or having a heterologous linker for a conjugated epitope in
CC (L), and containing a Cys residue at, or near, the C-terminus that
CC confers enhanced stability to the particles. A vaccine comprising (I) is
CC useful for inducing an immune response in an inoculated host animal, by
CC inoculating a host animal with the vaccine, and maintaining that
CC inoculated animal for a time period sufficient for that animal to develop
CC an immune response. The immunogenic particles formed using (I) are
CC substantially free of binding to nucleic acids, and are most stable than
CC the particle formed from otherwise identical Hbc chimera that lacks the C-
CC terminal residue or in which a C-terminal Cys is replaced by another
CC residue. The chimera particles are most stable on storage in aqueous
CC compositions that are particles of similar sequence that lack any C-
CC terminal Cys residues. The chimera molecule exhibits the self-assembly not
CC exhibiting the nucleic acid binding of those native particles, and
CC excellent B cell and T cell immunogenicities. The chimera particles are
CC typically prepared in higher yield than similar particles that are free
CC of a C-terminal Cys. The particles are often far more immunogenic than
CC the similar conjugates that lack a C-terminal Cys. Immunogenicities of
CC similar particles assembled from the chimera molecules are enhanced as compared to
CC particles assembled from chimera molecules lacking at least one C-
CC terminal Cys. AAU93802-AAU93997 represent immunogenic Hbc particles amino
CC acid sequences and related sequences of the invention
XX
SQ Sequence 183 AA;
Query Match 100.0%; Score 793; DB 5; Length 183;
Best Local Similarity 100.0%; Pred. No. 9.7e-85;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALQAIL 60
Db 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALQAIL 60
Qy 61 CWGELMTLATWGVNLEDPASRDVLVSVYNTNMGLKFRQLLWFHISCLTFGRETVEYLV 120
Db 61 CWGELMTLATWGVNLEDPASRDVLVSVYNTNMGLKFRQLLWFHISCLTFGRETVEYLV 120
Qy 121 SFGVWIRTPPAYRPPNAPILSTLPETTIV 149
Db 121 SFGVWIRTPPAYRPPNAPILSTLPETTIV 149
RESULT 7
ABG80494
ID ABG80494 standard; protein; 183 AA.
XX
XX ABG80494;
AC
XX

DT XX 29-NOV-2002 (first entry)
DE XX Hepatitis B virus core capsid protein, HBcAg, variant #11.
KW Molecular antigen array; vaccine; antigen; antimicrobial;
KW molecular scaffold; amyloid beta; Abeta 1-42; influenza;
KW graft versus host disease; Igb-mediated allergic reaction; anaphylaxis;
KW adult respiratory distress syndrome; ARDS; Crohn's disease;
KW allergic asthma; acute lymphoblastic leukaemia; non-Hodgkin's lymphoma;
KW Grave's disease; systemic lupus erythematosus; osteoporosis;
KW inflammatory immune disease; myasthenia gravis; multiple sclerosis;
KW immunoproliferative disease lymphadenopathy; Alzheimer's disease;
KW angioimmunoproliferative lymphadenopathy; immunoblastic lymphadenopathy;
KW rheumatoid arthritis; diabetes; infectious disease; factor Xa;
KW enterokinase; cysteine-containing linker.
XX OS Hepatitis B virus.
XX PD WO200256907-A2.
XX 25-JUL-2002.
XX 21-JAN-2002; 2002WO-IB000168.
XX 19-JAN-2001; 2001US-0262379P.
XX 04-MAY-2001; 2001US-0288549P.
XX 05-OCT-2001; 2001US-0326998P.
XX 07-NOV-2001; 2001US-0331045P.
XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX (NOV) NOVARTIS PHARMA AG.
XX (MAUR) MAURER P.
XX (LECH) LECHNER F.
XX (ORTM) ORTMANN R.
XX (LUEO) LUEOEND R.
XX (STAU) STAUFENBIEL M.
XX (FREY) FREY P.
XX Maurer P, Lechner F, Ortmann R, Lueoend R, Staufenbiel M, Frey P;
PI Renner WA, Bachmann M, Tissot A, Sebbel P, Piossek C;
XX WPI; 2002-636514/68.
XX Molecular antigen array used in the production of vaccines for infectious
XX diseases.
XX Claim 14; Page 314-315; 418pp; English.
XX The invention relates to a composition comprising: (a) a non-natural
XX molecular scaffold comprising: (i) a core particle selected from: (1) a
XX core particle of a non-natural origin; and (2) a core particle of natural
XX origin; and (ii) an organiser comprising at least one first attachment
XX site, where the organiser is connected to the core particle by at least
XX one covalent bond; (b) an antigen or antigenic determinant with at least
XX one second attachment site, where the antigen or antigenic determinant is
XX amyloid beta peptide (Abeta 1-42) or its fragment, and where the second
XX attachment site is selected from: (i) an attachment site not naturally
XX occurring with the antigen or antigenic determinant; and (ii) an
XX attachment site naturally occurring with the antigen or antigenic
XX determinant, where the second attachment site is capable of association
XX through at least one non-peptide bond to the first attachment site; and
XX where the antigen or antigenic determinant and the scaffold interact
XX through the association to form an ordered and repetitive antigen array.
XX Also included is a process for producing a non-naturally occurring
XX ordered and repetitive antigen array. The composition is used in
XX immunisation and as a vaccine for diseases such as influenza. Graft
XX versus host disease, Igb-mediated allergic reactions, anaphylaxis, adult
XX respiratory distress syndrome (ARDS), Crohn's disease, allergic asthma,
XX acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's disease,
XX systemic lupus erythematosus, inflammatory immune diseases, myasthenia
XX gravis, immunoproliferative disease lymphadenopathy,
XX angioimmunoproliferative lymphadenopathy, immunoblastic lymphadenopathy,
XX rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's disease,
XX

CC osteoporosis and infectious diseases. The present sequence is an antigen
CC for use in the array of the invention. The antigen is modified to possess
CC a cleavage site (enterokinase or factor Xa) and a Cysteine- containing N-
CC or C-terminal linker peptide which serves as the attachment point to a
CC virus like particle or bacterial protein (the scaffold protein)
XX SQ Sequence 183 AA;
Query Match 100.0%; Score 793; DB 5; Length 183;
Best Local Similarity 100.0%; Pred. No. 9.7e-85;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDIDPYKEGATVELLSFLPSPDFPSVRLDLDTSALYREALESPHCHSPHTALRQAIL 60
Db 1 MDIDPYKEGATVELLSFLPSPDFPSVRLDLDTSALYREALESPHCHSPHTALRQAIL 60
QY 61 CWGELMTLATWGVNLEDPASRDLDVSVYNTNMGLKFRQLLMFHFISCLTFGRETVEIYLV 120
Db 61 CWGELMTLATWGVNLEDPASRDLDVSVYNTNMGLKFRQLLMFHFISCLTFGRETVEIYLV 120
QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVV 149
Db 121 SFGVWIRTPPAYRPPNAPILSTLPETTVV 149

RESULT 8

AB001919
ID ABO01919 standard; protein; 183 AA.
XX AC ABO01919;
XX DT 07-AUG-2003 (first entry)
XX DE Hepatitis B virus core protein antigen.
XX KW Cholesteryl ester transfer protein; CETP; HDL cholesterol;
XX high density lipoprotein; immunogen; pro-atherogenic dyslipoproteinaemia;
XX low density lipoprotein; LDL; HBcAg; hepatitis core antigen.
XX OS Hepatitis B virus.
XX PN US2003021804-A1.
XX PD 30-JAN-2003.
XX PF 21-JAN-1997; 97US-00785997.
XX PR 21-JAN-1997; 97US-00785997.
XX (NEED/) NEEDLEMAN P.
XX (GLEN/) GLENN K.
XX PI Needleman P, Glenn K;
XX WPI; 2003-456282/43.
XX DR N-PSDB; ACD07806.
XX PT Increasing high density lipoprotein cholesterol level in blood of a
XX mammal whose blood contains cholesteryl ester transfer protein, by
XX PT immunizing mammal with inoculum of cholesteryl ester transfer protein
XX immunogen.
XX PS Disclosure; Page 30; 35pp; English.
XX CC The invention relates to increasing high density lipoprotein (HDL)
XX cholesterol in the blood of a mammal whose blood contains cholesteryl
XX ester transfer protein (CETP), comprising immunising mammal with an
XX inoculum having CETP immunogen that is an immunogenic polypeptide (IP)
XX having CETP amino acid residue sequence, allowing IP to induce production
XX of anti-CETP antibodies in mammal and lessen transfer of cholesteryl
XX esters from HDL. Also included is a CETP immunogen that comprises an
XX immunogenic polypeptide having a CETP amino acid residue sequence
XX covalently bonded to an exogenous antigenic carrier (e.g. hepatitis B

core protein antigen, HBcAg). The method is useful for increasing the concentration of HDL cholesterol in the blood of a mammal whose blood contains CETP. The method is useful for ameliorating or treating atherogenic dyslipoproteinaemias characterised by low HDL/low density lipoprotein (LDL) cholesterol ratios. The method has an effect that lasts for months as compared to the short-term effects of the small molecule drugs not available. The method utilises the host mammal's own (autogenic) immunological system to provide a desired result, thus obviating problems associated with repeated administration of xenogeneic antibodies that themselves become immunogenic in the host mammal. The method utilises accepted exogenous antigenic carriers such as hepatitis B core protein (HBcAg), tetanus toxoid, tuberculin purified protein derivative (PPD) and diphtheria toxoid which can boost the host mammal's immunity to those pathogens. The method also lessens the cholesterol ester transfer from HDL to LDL or very low density lipoprotein, thus increasing the concentration of anti-atherogenic HDL cholesterol. The present sequence represents the hepatitis B core protein (HBcAg) used as the exogenous antigenic carrier

Sequence 183 AA;

Query Match 100.0%; Score 793; DB 6; Length 183;
Best Local Similarity 100.0%; Pred. No. 9.7e-85;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIDPKFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHTALRQAIL 60
DB 1 MDIDPKFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHTALRQAIL 60
QY 61 CWGELMTLATWGVNLEDPASRDVSVYNTNMGLKFRQLLWFHISCLTFGRVTVYLV 120
DB 61 CWGELMTLATWGVNLEDPASRDVSVYNTNMGLKFRQLLWFHISCLTFGRVTVYLV 120
QY 121 SFGWIRTPPAYRPPNAPILSTLPETTVV 149
DB 121 SFGWIRTPPAYRPPNAPILSTLPETTVV 149

RESULT 9

ID ABR56468 standard; protein; 183 AA.

XX ABR56468;
AC ABR56468;

XX 28-JUL-2003 (first entry)

XX Hepatitis B core antigen precursor variant protein SEQ ID NO:39.

XX Antigen presenting cell; APC; immune response; virus like particle; VLP;
KW cytostatic; virucide; antibacterial; antiparasitic; fungicide;
KW antiallergic; immunosuppressive; antiaddictive; antiinflammatory;
KW antichyroid; antidiabetic; neuroprotective; nontropic; osteopathic;
KW antirheumatic; antiarthritic; vaccine; immunisation; infectious disease;
KW anti-viral protection; tumour; allergy; drug addiction; Crohn's disease;
KW graft-versus-host disease; Grave's disease; diabetes; multiple sclerosis;
KW Alzheimer's disease; osteoporosis; rheumatoid arthritis;
KW inflammatory autoimmune disease.

XX Hepatitis B virus.
OS Synthetic.

XX WO2003024480-A2.

XX 27-MAR-2003.

XX 16-SEP-2002; 2002WO-IB004252.

XX 14-SEP-2001; 2001US-0318967P.

XX (CYTO-) CYTOS BIOTECHNOLOGY AG.

XX Bachmann MF, Storni T, Lechner F;

DR MPI; 2003-363095/34.

XX A composition, useful for enhancing an immune response against an antigen or a virus-like particle, enhancing anti-viral protection in an animal, PT or immunizing or treating tumors or infectious diseases, e.g. viral PT infections.

PS Disclosure; Page 195; 243pp; English.

XX The present invention describes a composition (C) for enhancing an immune response against an antigen or a virus-like particle in an animal. (C) comprises a virus-like particle (VLP) bound to at least one antigen, or a VLP capable of being recognised by the immune system of the animal. Also described: (1) enhancing an immune response against an antigen or a VLP in an animal comprising introducing (C) into the animal; (2) vaccines comprising (C) together with a pharmaceutical diluent, carrier or excipient; (3) immunising or treating an animal comprising administering the vaccine to the animal, or priming or boosting a T cell response in the animal by administering the vaccine; and (4) enhancing anti-viral protection in an animal comprising introducing (C) into the animal. (C) has cytostatic, virucide, antibacterial, antiparasitic, fungicide, antiallergic, immunosuppressive, antiaddictive, antiinflammatory, CC antithyroid, antidiabetic, neuroprotective, nontropic, osteopathic, CC antirheumatic and antiarthritic activities. (C) or the vaccines can be used for enhancing an immune response against an antigen or a VLP in an animal, enhancing anti-viral protection in an animal, or immunising or treating tumors and infectious diseases such as viral, bacterial, parasitic or fungal infections. The vaccine compositions are also useful for preventing or treating allergies, drug addiction, graft-versus-host disease, Crohn's disease, Grave's disease, diabetes, multiple sclerosis, Alzheimer's disease, osteoporosis, rheumatoid arthritis, or inflammatory autoimmune disease. ACC69838 to ACC69852 and ABR56401 to ABR56509 CC represent sequences used in the exemplification of the present invention

XX Sequence 183 AA;

Query Match 100.0%; Score 793; DB 6; Length 183;
Best Local Similarity 100.0%; Pred. No. 9.7e-85;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIDPKFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHTALRQAIL 60

DB 1 MDIDPKFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHTALRQAIL 60

QY 61 CWGELMTLATWGVNLEDPASRDVSVYNTNMGLKFRQLLWFHISCLTFGRVTVYLV 120

DB 61 CWGELMTLATWGVNLEDPASRDVSVYNTNMGLKFRQLLWFHISCLTFGRVTVYLV 120

QY 121 SFGWIRTPPAYRPPNAPILSTLPETTVV 149

DB 121 SFGWIRTPPAYRPPNAPILSTLPETTVV 149

RESULT 10

ABR44571

ID ABR44571 standard; protein; 183 AA.

XX ABR44571;

XX 25-JUL-2003 (first entry)

XX Hepatitis B core antigen precursor variant protein SEQ ID NO:39.

XX Immunostimulatory; virus-like particle; bacteriophage; HBV; LCMV;
KW hepatitis B virus; lymphocytic choriomeningitis virus; vaccine;
KW immunostimulant; cytostatic; antiaddictive; antiinflammatory;
KW immune response; immunisation; allergy; tumour; breast cancer;
KW neuroblastoma; leukaemia; viral disease; influenza; hepatitis; measles;
KW chicken pox; bacterial infection; tuberculosis; pneumonia; syphilis.

XX Hepatitis B virus.

OS Synthetic.

XX

PN WO2003024481-A2.
XX 27-MAR-2003.
PD 16-SEP-2002; 2002WO-IB004132.
XX 14-SEP-2001; 2001US-0318994P.
XX 22-APR-2002; 2002US-0374145P.
XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
PA (MAUR-) MAURER P.
PA (TISS-) TISSOT A.
PA (SCHW-) SCHWARZ K.
PA (MEIJ-) MEIJERINK E.
PA (LIPO-) LIPOWSKY G.
PA (PUMP-) PUMPKENS P.
PA (CIEL-) CIELENS I.
PA (RENH-) RENHOFA R.
XX Maurer P, Tisser A, Schwarz K, Meijerink E, Lipowsky G;
PI Pumpens P, Cielens I, Renhofs R, Bachmann MP, Storni T;
XX WPI: 2003-354564/33.
XX New compositions comprising immunostimulatory substances packaged into
PT virus-like particles, useful as a vaccine for enhancing an immune
PT response in animals, e.g. for treating or preventing allergies, tumors or
PT viral infections.
PS Disclosure; Page 274-275; 322pp; English.
XX The present invention describes a composition (C) for enhancing an immune
CC response in an animal. (C) comprises a virus-like particle (VLP), and an
CC immunostimulatory substance. The immunostimulatory substance is bound to
CC the VLP. Also described: (1) enhancing an immune response in an animal by
CC introducing (C) into the animal; (2) producing (C) for enhancing an
CC immune response in an animal; (3) vaccines comprising (C) together with a
CC pharmaceutical diluent, carrier or excipient; and (4) immunising or
CC treating an animal by: (a) administering the vaccine to the animal; (b)
CC priming a T cell response in the animal by administering the vaccine; or
CC (c) boosting a T cell response in the animal by administering the
CC vaccine. (C) has immunostimulant, cytostatic, antiallergic, virucide and
CC antibacterial activities. (1) can be used in vaccines for enhancing an
CC immune response in an animal, particularly a mammal or human.
CC Specifically, (C) is useful for enhancing a B cell response, a T cell
CC response, or a cytotoxic T-lymphocyte (CTL) response. (C) or a vaccine
CC comprising (C) can also be used for immunising or treating an animal,
CC e.g. humans, sheep, horses, cattle, pigs, dogs, cats, rats, birds,
CC reptiles or fish. (C) is particularly useful in prophylactic or
CC therapeutic vaccines against allergies, tumors (e.g. breast cancers,
CC neuroblastoma, or leukaemia), viral diseases (e.g. influenza, hepatitis,
CC measles or chicken pox), or bacterial infections (e.g. tuberculosis,
CC pneumonia or syphilis). ACC69790 to ACC69815 and ABR44502 to ABR44612
XX represent sequences used in the exemplification of the present invention
SQ Sequence 183 AA;
Query Match 100.0%; Score 793; DB 6; Length 183;
Best Local Similarity 100.0%; Pred. No. 9,7e-85;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALROAIL 60
Db 1 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALROAIL 60
QY 61 CWGELMTLATWGVNLEDPSARDLVSVYNTNMGLKFRQLLWFIHISCLTFTGRTVIEYLV 120
Db 61 CWGELMTLATWGVNLEDPSARDLVSVYNTNMGLKFRQLLWFIHISCLTFTGRTVIEYLV 120
QY 121 SFGWIRTTPAYRPPNAPILSTLPETTV 149
Db 121 SFGWIRTTPAYRPPNAPILSTLPETTV 149

RESULT 11
ADD24146
ID ADD24146 standard; protein; 183 AA.
XX AC ADD24146;
XX 15-JAN-2004 (first entry)
DT Hepatitis B virus core antigen (HBcAg) precursor variant Seq ID39.
XX vaccine composition; virus-like particle; core particle;
XX first attachment site; antigen; antigenic determinant; prion protein;
KW PrP; PrP peptide; vaccine; neuroprotective; antiinflammatory;
KW Prion disease; Bovine Spongiform Encephalopathy; BSE;
KW Creutzfeldt-Jakob Disease; HBcAg; mutant; mutein.
XX Hepatitis B virus.
XX WO2003059386-A2.
XX 24-JUL-2003.
XX 17-JAN-2003; 2003WO-EP000460.
XX 18-JAN-2002; 2002US-00050902.
XX 21-JAN-2002; 2002WO-IB000166.
XX 08-JUL-2002; 2002US-0393725P.
XX 18-JUL-2002; 2002US-0396590P.
XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX Bachmann M, Maurer P, Pelliccioli E, Renner WA;
XX WPI: 2003-598493/56.
XX A vaccine composition for preventing or treating prion diseases (e.g.
PT Creutzfeldt-Jakob Disease) comprises a virus-like particle (e.g. RNA-
PT phase) and at least one prion protein or peptide bound to the virus-like
PT particle.
XX Disclosure; SEQ ID NO 39; 246pp; English.
XX This invention relates to a novel vaccine composition comprising a virus-
XX like or a core particle with at least one first attachment site and at
XX least one antigen or antigenic determinant that is a prion protein (PrP)
XX or its dimer, or a PrP peptide, the antigen or antigenic determinant
XX being bound to the virus-like or core particle. The vaccine of the
XX invention may have neuroprotective or antiinflammatory activity. The
XX composition is useful as a medicament or in manufacturing a medicament
XX for the treatment or prevention of prion diseases. The prion diseases may
XX include Bovine Spongiform Encephalopathy (BSE) or Creutzfeldt-Jakob
XX Disease. The present sequence is the amino acid sequence of a mutant
XX hepatitis B virus core antigen (HBcAg) which may be used during the
XX creation of the vaccine composition of the invention.
SQ Sequence 183 AA;
Query Match 100.0%; Score 793; DB 7; Length 183;
Best Local Similarity 100.0%; Pred. No. 9,7e-85;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALROAIL 60
Db 1 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALROAIL 60
QY 61 CWGELMTLATWGVNLEDPSARDLVSVYNTNMGLKFRQLLWFIHISCLTFTGRTVIEYLV 120
Db 61 CWGELMTLATWGVNLEDPSARDLVSVYNTNMGLKFRQLLWFIHISCLTFTGRTVIEYLV 120
QY 121 SFGWIRTTPAYRPPNAPILSTLPETTV 149
Db 121 SFGWIRTTPAYRPPNAPILSTLPETTV 149

RESULT 12

AD10767
 ID ADE10767 standard; protein; 183 AA.
 AC ADE10767;
 DT 29-JAN-2004 (first entry)
 XX
 DE Human Hepatitis B virus sub-type AYW core protein.
 KW hepatotropic; virucide; antiinflammatory; chronic hepatitis; vaccine;
 KW recombinant hepatitis B core chimeric protein; Hbc chimeric protein;
 KW hepatitis B infection; T-cell stimulator.
 XX
 OS Hepatitis B virus.
 XX
 PN US2003198645-A1.
 XX
 PD 23-OCT-2003.
 XX
 PF 21-FEB-2003; 2003US-00372076.
 XX
 PR 21-FEB-2002; 2002US-00080299.
 PR 21-FEB-2002; 2002US-00082014.
 XX
 PA (PAGE/) PAGE M.
 PA (FRIE/) FRIEDE M.
 XX
 PI Page M, Friede M;
 XX
 DR WPI; 2003-852775/79.
 DR N-PSDB; ADE10968.
 XX
 PT Treating chronic hepatitis B infection by administering a T cell-
 PT stimulating vaccine containing immunogenic particles having recombinant
 PT carboxy-terminal truncated hepatitis B core (Hbc) chimeric protein
 PT molecules.
 XX
 PS Claim 18; SEQ ID NO 1; 111pp; English.
 XX
 CC The invention describes a method of treating chronic hepatitis comprising
 CC administering to a patient a T cell-stimulating amount of a vaccine
 CC comprising immunogenic particles dissolved or dispersed in a diluent,
 CC where the immunogenic particles consists of recombinant hepatitis B core
 CC (Hbc) chimeric protein molecules, and maintaining the patient to induce T
 CC cells activated against Hbc. The methods and compositions of the present
 CC invention are useful for treating chronic hepatitis B infection. This is
 CC the amino acid sequence of a Hepatitis B core protein.
 XX
 SQ Sequence 183 AA;
 Query Match 100.0%; Score 793; DB 7; Length 183;
 Best Local Similarity 100.0%; Pred. No. 9.7e-85;
 Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHPTALRQAIL 60
 DB 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHPTALRQAIL 60
 QY 61 CWGELMTLATWGVNLEDPASRDVLVSYVNTNMGKFRQLLWPHISCLTFGRETVEYL 120
 DB 61 CWGELMTLATWGVNLEDPASRDVLVSYVNTNMGKFRQLLWPHISCLTFGRETVEYL 120
 QY 121 SFGWIRTPPAYRPPNAPILSTLPTTVV 149
 DB 121 SFGWIRTPPAYRPPNAPILSTLPTTVV 149
 RESULT 13
 AAW50242
 ID AAW50242 standard; protein; 194 AA.

XX AAW50242;
 AC
 DT 28-SEP-1998 (first entry)
 XX
 DE Hepatitis B virus precore p22 polypeptide Met-p22.
 XX
 KW Viral replication; inhibitor; HBV; nucleocapsid; gene therapy;
 KW hepatocyte; liver; Met-p22.
 XX
 OS Hepatitis B virus.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Protein 2..194
 FT /label= p22
 XX
 PN WO9809649-A1.
 XX
 PD 12-MAR-1998.
 XX
 PF 03-SEP-1997; 97WO-US015500.
 XX
 PR 03-SEP-1996; 96US-0025370P.
 XX
 PA (GEO) GEN HOSPITAL CORP.
 XX
 PI Wands JR, Scaglioni PP, Melegari M;
 XX
 DR WPI; 1998-193325/17.
 XX
 PT DNA encoding proteins which can be incorporated with wild type
 PT nucleocapsid subunit(s) into a viral nucleocapsid - useful for
 PT inhibition of viral replication, especially hepatitis B virus.
 XX
 PS Claim 11; Page 40; 60pp; English.
 XX
 CC This polypeptide comprises the hepatitis B virus (HBV) 22 kDa (p22)
 CC protein with an added N-terminal Met residue. p22 is produced by
 CC elimination of the 19-amino acid leader peptide from the 25 kDa full-
 CC length HBV precore protein (see AAW50250). Evidence is provided that HBV
 CC replication is inhibited in the presence of high levels of HBV precore or
 CC precore-related proteins. These proteins can be incorporated into HBV
 CC nucleocapsids along with the p21 core protein (see AAW50251), which is
 CC the usual nucleocapsid component, and thereby render the nucleocapsids
 CC deficient in encapsidating HBV pregenomic RNA. Thus, over-expression of
 CC the precore proteins, or certain variants of them, leads to transdominant
 CC inhibition of HBV replication. Suitable inhibitory proteins include p25
 CC (see AAW50250), p22, Met-p22, p18 (see AAW50236), Met-p18 (see AAW50237)
 CC and Met-p18-Het (see AAW50238). Heterologous peptides (see AAW50244-49)
 CC may be inserted into the p22 and Met-p22 polypeptides. The inhibitory
 CC proteins can be produced by recombinant methods using claimed expression
 CC vectors and host cells. They can be provided exogenously to the target
 CC cells for use in inhibiting HBV replication. Alternatively, a nucleic
 CC acid construct that directs overexpression of an inhibitory protein in
 CC target cells is used for the gene therapy of HBV infection
 XX
 SQ Sequence 194 AA;
 Query Match 100.0%; Score 793; DB 2; Length 194;
 Best Local Similarity 100.0%; Pred. No. 1e-84;
 Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHPTALRQAIL 60
 DB 12 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHPTALRQAIL 71
 QY 61 CWGELMTLATWGVNLEDPASRDVLVSYVNTNMGKFRQLLWPHISCLTFGRETVEYL 120
 DB 72 CWGELMTLATWGVNLEDPASRDVLVSYVNTNMGKFRQLLWPHISCLTFGRETVEYL 131
 QY 121 SFGWIRTPPAYRPPNAPILSTLPTTVV 149
 |||||

Db 132 SFGWIRTPPAYRPPNAPILSTLPTTVV 160

RESULT 14

AAW50250
ID AAW50250 standard; protein; 212 AA.

XX AC AAW50250;

XX DT 28-SEP-1998 (first entry)

XX DE Hepatitis B virus precore p25 polypeptide.

XX KW Viral replication; inhibitor; HBV; nucleocapsid; gene therapy;
XX KW hepatocyte; liver; p25 protein.

XX OS Hepatitis B virus.

XX PN WO9809649-A1.

XX PD 12-MAR-1998.

XX PF 03-SEP-1997; 97WO-US015500.

XX PR 03-SEP-1996; 96US-0025370P.

XX PA (GEO) GEN HOSPITAL CORP.

XX PI Wands JR, Scaglioni PP, Melegari M;

XX DR WPI; 1998-193325/17.

XX PT DNA encoding proteins which can be incorporated with wild type
XX PT nucleocapsid sub-unit(s) into a viral nucleocapsid - useful for
XX PT inhibition of viral replication, especially hepatitis B virus.

XX PS Claim 15; Page 35; 60pp; English.

XX CC This polypeptide comprises the hepatitis B virus (HBV) 25 kDa (p25)
XX CC protein that is encoded by the full-length HBV precore gene. Evidence is
XX CC provided that HBV replication is inhibited in the presence of high levels
XX CC of HBV precore or precore-related proteins. These proteins can be
XX CC incorporated into HBV nucleocapsids along with the p21 core protein (see
XX CC AAW50251), which is the usual nucleocapsid component, and thereby render
XX CC the nucleocapsids deficient in encapsidating HBV pregenomic RNA. Thus,
XX CC over-expression of the precore proteins, or certain variants of them,
XX CC leads to transdominant inhibition of HBV replication. Suitable inhibitory
XX CC proteins include p25, p22 (see AAW50241), Met-p22 (see AAW50242), p18
XX CC (see AAW50236), Met-p18 (see AAW50237) and Met-p18-Het (see AAW50238).
XX CC The inhibitory proteins can be produced by recombinant methods using
XX CC claimed expression vectors and host cells. They can be provided
XX CC exogenously to the target cells for use in inhibiting HBV replication.
XX CC Alternatively, a nucleic acid construct that directs overexpression of an
XX CC inhibitory protein in target cells is used for the gene therapy of HBV
XX CC infection

XX SQ Sequence 212 AA;

Query Match 100.0%; Score 793; DB 2; Length 212;
Best Local Similarity 100.0%; Pred. No. 1.2e-84;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIDPKKCATVLLSFLPSDFPSVRDLDTASALYREALESPHCSPHTALRQAIL 60
Db 30 MDIDPKKCATVLLSFLPSDFPSVRDLDTASALYREALESPHCSPHTALRQAIL 89
QY 61 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGKFRQLLWFHISCLTFTGRTVEIYL 120
Db 90 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGKFRQLLWFHISCLTFTGRTVEIYL 149
QY 121 SFGWIRTPPAYRPPNAPILSTLPTTVV 149
Db 150 SFGWIRTPPAYRPPNAPILSTLPTTVV 178

RESULT 15

AAU80921

ID AAU80921 standard; protein; 212 AA.

XX AC AAU80921;

XX DT 09-APR-2002 (first entry)

XX DE Hepatitis B virus core antigen variant (HBCAg) #26.

XX KW Vaccine; molecular scaffold; pilus; pilin; HBCAg; antigen;
XX KW hepatitis B virus capsid protein; JUN; FOS; HIV gp140;
XX KW measles virus N protein; bee venom phospholipase; Th type 2 T-helper;
XX KW Th2; Sinbis virus E2 protein; amyloid beta; influenza M2 antigen;
XX KW human immunodeficiency virus infection; viral hepatitis; measles;
XX KW chicken pox; pneumonia; tuberculosis; syphilis; malaria; allergy; cancer;
XX KW chronic disease; arthritis; colitis; diabetes; multiple sclerosis.

XX OS Hepatitis B virus.

XX PN WO200185208-A2.

XX PD 15-NOV-2001.

XX PF 02-MAY-2001; 2001WO-IB000741.

XX PR 05-MAY-2000; 2000US-0202341P.

XX PA (CYTO-) CYTOS BIOTECHNOLOGY AG.

XX PA (SEBB) SEBBEL P.

XX PA (DUNA) DUNANT N.

XX PA (BACH) BACHMANN M.

XX PA (TISS) TISSOT A.

XX PA (LECH) LECHENER F.

XX PI Sebbel P, Dunant N, Bachmann M, Tissot A, Lechener F;

XX DR WPI; 2002-055561/07.

XX PT New composition, useful for vaccine production, comprises antigen or
XX PT antigenic determinant and non-natural molecular scaffold comprising
XX PT organizer and core particle such as bacterial pilus or pilin protein.

XX PS Disclosure; Page 227-228; 287pp; English.

XX CC The invention relates to a composition comprising: (a) a non-natural
XX CC molecular scaffold (molecular scaffold) which comprises a core particle
XX CC such as a bacterial pilus or pilin protein, a recombinant form of the
XX CC protein, a virus-like particle or a hepatitis B virus capsid protein
XX CC (HBCAg), and an organizer, and (b) an antigen or antigenic determinant,
XX CC where the molecular scaffold and antigenic determinant interact to form
XX CC an ordered and repetitive antigen array. Suitable antigenic determinants
XX CC include JUN, FOS, HIV gp140, measles virus N protein, bee venom
XX CC phospholipase, Sinbis virus E2 protein, amyloid beta derived peptides and
XX CC influenza M2 antigen. The composition (or vaccine) is useful for
XX CC immunisation, by administration to a subject, where the administration
XX CC produces an immune response, such as humoral, cellular or protective
XX CC immune response, preferably a Th type 2 T-helper (Th2) response that is
XX CC specific for the antigenic determinant. The administration induces
XX CC antibodies specific for the antigenic determinant of a subtype
XX CC corresponding to the Th2 subtype in the subject. The subject does not
XX CC generate a Th2 subtype that is specific for pilus or pilin polypeptide or
XX CC antigenic determinant. The composition is useful for the production of
XX CC vaccines for prevention of infectious diseases such as human
XX CC immunodeficiency virus, viral hepatitis, measles, chicken pox, pneumonia,
XX CC tuberculosis, syphilis, malaria, and for treating allergy, cancer, and
XX CC chronic diseases induced or accelerated by a Th1 type immune response,
XX CC such as arthritis, colitis, diabetes and multiple sclerosis. The
XX CC composition is useful to generate defined self-specific antibodies and
XX CC specific immune responses of the Th2 type and allows the creation of
XX CC highly efficient vaccines against infectious diseases, and for treating

CC allergy, cancer, and chronic diseases induced or accelerated by a Th1
CC type immune response. The present sequence is a peptide or protein
CC incorporated into the compositions of the invention

XX
SQ Sequence 212 AA;
Query Match 100.0%; Score 793; DB 5; Length 212;
Best Local Similarity 100.0%; Pred. No. 1.2e-84;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALESPHCSPHHTALRQAIL 60
Db 30 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALESPHCSPHHTALRQAIL 89
QY 61 CWGELMTLATWGVNLEDPASRDLVVSYVNTNMGKFRQLLWPHFHSCLTFGRETVEYLV 120
Db 90 CWGELMTLATWGVNLEDPASRDLVVSYVNTNMGKFRQLLWPHFHSCLTFGRETVEYLV 149
QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTV 149
Db 150 SFGVWIRTPPAYRPPNAPILSTLPETTV 178

Search completed: April 23, 2004, 16:28:16
Job time : 58 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 23, 2004, 16:27:14 ; Search time 23 Seconds
(without alignments)
334.447 Million cell updates/sec

Title: US-09-931-325c-170_COPY_1_149

Perfect score: 793
Sequence: 1 MDIDPKFGATVELLSFLP.....PAYRPPNAPILSLPPTTVV 149

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pap:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pap:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pap:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pap:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pap:*
6: /cgn2_6/ptodata/2/iaa/backfiles.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	793	100.0	159	3	US-08-445-585-3
2	793	100.0	183	3	US-09-248-588-2
3	793	100.0	194	3	US-08-968-747-18
4	793	100.0	212	3	US-08-968-747-3
5	793	100.0	212	4	US-10-104-966-11
6	793	100.0	289	5	PCT-US96-10602-8
7	793	100.0	346	1	US-08-105-483-217
8	793	100.0	346	1	US-08-709-209-217
9	793	100.0	346	1	US-08-458-101-217
10	793	100.0	397	5	PCT-US96-10602-6
11	787	99.2	183	5	PCT-US96-10602-12
12	785	99.0	351	5	PCT-US96-10602-4
13	778	98.1	183	3	US-08-968-747-20
14	778	98.1	193	3	US-08-968-747-2
15	775	97.7	185	1	US-07-739-642-2
16	775	97.7	185	1	US-07-739-643-2
17	775	97.7	185	1	US-07-739-142-2
18	775	97.7	185	4	US-09-851-120-6
19	772	97.4	185	3	US-09-248-588-6
20	771	97.2	185	1	US-07-739-642-4
21	771	97.2	185	1	US-07-739-643-4
22	771	97.2	185	1	US-07-739-142-4
23	770	97.1	184	3	US-08-968-747-1
24	770	97.1	185	3	US-08-968-747-17
25	770	97.1	161	3	US-08-968-747-21
26	767.5	96.8	199	3	US-08-968-747-21
27	767	96.7	214	1	US-07-739-642-12

28	767	96.7	214	1	US-07-739-643-12
29	767	96.7	214	1	US-07-739-142-12
30	763	96.2	185	1	US-07-739-642-10
31	763	96.2	185	1	US-07-739-643-10
32	763	96.2	185	1	US-07-739-142-10
33	760	95.8	183	3	US-09-248-588-4
34	760	95.8	185	1	US-07-739-642-8
35	760	95.8	185	1	US-07-739-643-8
36	760	95.8	185	1	US-07-739-142-8
37	757	95.5	214	1	US-07-739-642-6
38	757	95.5	214	1	US-07-739-643-6
39	757	95.5	214	1	US-07-739-142-6
40	746	94.1	212	4	US-09-719-528A-4
41	734.5	92.6	211	6	5196194-13
42	538	67.8	188	3	US-09-248-588-7
43	534.5	67.4	217	3	US-09-248-588-9
44	529	66.7	346	5	PCT-US96-10602-2
45	132	16.6	305	3	US-09-248-588-11

ALIGNMENTS

RESULT 1
US-08-445-585-3
; Sequence 3, Application US/08445585
; Patent No. 6277631
; GENERAL INFORMATION:
; APPLICANT: No. 6277631h, Michael
; APPLICANT: Broeker, Michael
; TITLE OF INVENTION: Recombinant Proteins with the
; TITLE OF INVENTION: Immunoreactivity of Hepatitis B Virus E Antigen (HBeAg), A
; TITLE OF INVENTION: Process for the Preparation Thereof and the Use Thereof in
; TITLE OF INVENTION: Immunoassays and Vaccines
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/445,585
; FILING DATE: 22-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/846,194
; FILING DATE: 06-MAR-1992
; APPLICATION NUMBER: DE P 41 07 612.5
; FILING DATE: 03-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Ogden, Stasia L.
; REGISTRATION NUMBER: P-36,228
; REFERENCE/DOCKET NUMBER: 02481.1162-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 159 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-445-585-3

Query Match 100.0%; Score 793; DB 3; Length 159;

Best Local Similarity 100.0%; Pred. No. 3.1e-87; Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCHSPHHTALRAIL 60
DB 11 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCHSPHHTALRAIL 70
QY 61 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGKFRQLLWFHISCLTFGRETVEIYLV 120
DB 71 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGKFRQLLWFHISCLTFGRETVEIYLV 130
QY 121 SFGWIRTTPPAYRPPNAPILSTLPETTVV 149
DB 131 SFGWIRTTPPAYRPPNAPILSTLPETTVV 159

RESULT 2
US-09-248-588-2
; Sequence 2, Application US/09248588
; Patent No. 6231864
; GENERAL INFORMATION:
; APPLICANT: Birkett, Ashley J.
; TITLE OF INVENTION: Strategically Modified Hepatitis B Core Proteins and
; TITLE OF INVENTION: their Derivatives
; FILE REFERENCE: SYN-101 4564/69529
; CURRENT APPLICATION NUMBER: US/09/248,588
; CURRENT FILING DATE: 1999-02-11
; EARLIER APPLICATION NUMBER: 60/074537
; EARLIER FILING DATE: 1998-02-12
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-09-248-588-2

Query Match 100.0%; Score 793; DB 3; Length 183;
Best Local Similarity 100.0%; Pred. No. 3.7e-87;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCHSPHHTALRAIL 60
DB 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCHSPHHTALRAIL 60
QY 61 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGKFRQLLWFHISCLTFGRETVEIYLV 120
DB 61 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGKFRQLLWFHISCLTFGRETVEIYLV 120
QY 121 SFGWIRTTPPAYRPPNAPILSTLPETTVV 149
DB 121 SFGWIRTTPPAYRPPNAPILSTLPETTVV 149

RESULT 3
US-08-968-747-18
; Sequence 18, Application US/08968747
; Patent No. 6060595
; GENERAL INFORMATION:
; APPLICANT: Scaglioni et al.
; TITLE OF INVENTION: INHIBITION OF VIRAL REPLICATION
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Windows
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/968,747
; FILING DATE: 03-SEP-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08472/705001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 212 amino acids

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/968,747
FILING DATE: 03-SEP-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 08472/705001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 194 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-968-747-18

Query Match 100.0%; Score 793; DB 3; Length 194;
Best Local Similarity 100.0%; Pred. No. 4.1e-87;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCHSPHHTALRAIL 60
DB 12 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCHSPHHTALRAIL 71
QY 61 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGKFRQLLWFHISCLTFGRETVEIYLV 120
DB 72 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGKFRQLLWFHISCLTFGRETVEIYLV 131
QY 121 SFGWIRTTPPAYRPPNAPILSTLPETTVV 149
DB 132 SFGWIRTTPPAYRPPNAPILSTLPETTVV 160

RESULT 4
US-08-968-747-3
; Sequence 3, Application US/08968747
; Patent No. 6060595
; GENERAL INFORMATION:
; APPLICANT: Scaglioni et al.
; TITLE OF INVENTION: INHIBITION OF VIRAL REPLICATION
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Windows
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/968,747
; FILING DATE: 03-SEP-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08472/705001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 212 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-968-747-3

Query Match 100.0%; Score 793; DB 3; Length 212;
Best Local Similarity 100.0%; Pred. No. 4.6e-87;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCHSPHHTALRQAIL 60
DB 30 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCHSPHHTALRQAIL 89
QY 61 CWGELMTLATWGVNLEDPASRDVLVSYNTNMGKFRQLLWFHISCLTFGRETVEIYLV 120
DB 90 CWGELMTLATWGVNLEDPASRDVLVSYNTNMGKFRQLLWFHISCLTFGRETVEIYLV 149
QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVV 149
DB 150 SFGVWIRTPPAYRPPNAPILSTLPETTVV 178

RESULT 5
US-10-104-966-11
Sequence 11, Application US/10104966
Patent No. 6880059
GENERAL INFORMATION:
APPLICANT: Matti Sallberg
APPLICANT: Catharina Hultgren
TITLE OF INVENTION: VACCINES CONTAINING RIBAVIRIN AND
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: TRIPEP 23AUSC1
CURRENT APPLICATION NUMBER: US/10/104,966
PRIOR FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: 09/705,547
PRIOR FILING DATE: 2000-11-03
PRIOR APPLICATION NUMBER: 60/229,175
PRIOR FILING DATE: 2000-08-29
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11
LENGTH: 212
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Hepatitis B virus C antigen and e antigen
OTHER INFORMATION: (HbcAg/HbeAg) sequence
US-10-104-966-11

Query Match 100.0%; Score 793; DB 4; Length 212;
Best Local Similarity 100.0%; Pred. No. 4.6e-87;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCHSPHHTALRQAIL 60
DB 30 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCHSPHHTALRQAIL 89
QY 61 CWGELMTLATWGVNLEDPASRDVLVSYNTNMGKFRQLLWFHISCLTFGRETVEIYLV 120
DB 90 CWGELMTLATWGVNLEDPASRDVLVSYNTNMGKFRQLLWFHISCLTFGRETVEIYLV 149
QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVV 149
DB 150 SFGVWIRTPPAYRPPNAPILSTLPETTVV 178

RESULT 6
PCT-US96-10602-8
Sequence 8, Application PC/TUS9610602
GENERAL INFORMATION:
APPLICANT: The General Hospital Corporation
TITLE OF INVENTION: INHIBITION OF HEPATITIS B REPLICATION
NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10602
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/017,814
FILING DATE: 20-JUN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/282001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 289 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-10602-8

Query Match 100.0%; Score 793; DB 5; Length 289;
Best Local Similarity 100.0%; Pred. No. 7.1e-87;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCHSPHHTALRQAIL 60
DB 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCHSPHHTALRQAIL 60
QY 61 CWGELMTLATWGVNLEDPASRDVLVSYNTNMGKFRQLLWFHISCLTFGRETVEIYLV 120
DB 61 CWGELMTLATWGVNLEDPASRDVLVSYNTNMGKFRQLLWFHISCLTFGRETVEIYLV 120
QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVV 149
DB 121 SFGVWIRTPPAYRPPNAPILSTLPETTVV 149

RESULT 7
US-08-105-483-217
Sequence 217, Application US/08105483
Patent No. 5494807
GENERAL INFORMATION:
APPLICANT: Fagietti, Enzo
TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
TITLE OF INVENTION: STRAIN
NUMBER OF SEQUENCES: 462
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford
ADDRESSEE: c/o William S. Frommer
STREET: 530 Fifth Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/105,483
FILING DATE: 12-AUG-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/847,951
FILING DATE: 06-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2400
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 217:
SEQUENCE CHARACTERISTICS:
LENGTH: 346 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-105-483-217

Query Match 100.0%; Score 793; DB 1; Length 346;
Best Local Similarity 100.0%; Pred. No. 9,1e-87;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
DB 164 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 223

QY 61 CWGELMTLATWGVNLEDPASRDLVVSYNTNMGKFRQLLWPHISCLTFGRETVEIYLV 120
DB 224 CWGELMTLATWGVNLEDPASRDLVVSYNTNMGKFRQLLWPHISCLTFGRETVEIYLV 283

QY 121 SFGWIRTPPAYRPPNAPILSTLPETTV 149
DB 284 SFGWIRTPPAYRPPNAPILSTLPETTV 312

RESULT 8
US-08-709-209-217
Sequence 217, Application US/08709209
Patent No. 5762938
GENERAL INFORMATION:
APPLICANT: Paoletti, Enzo
TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
TITLE OF INVENTION: STRAIN
NUMBER OF SEQUENCES: 462
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford
STREET: 530 Fifth Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,209
FILING DATE: 21-AUG-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/105,483
FILING DATE: 12-AUG-1993
APPLICATION NUMBER: US 07/847,951
FILING DATE: 06-MAR-1992
ATTORNEY/AGENT INFORMATION:

NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2400
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 217:
SEQUENCE CHARACTERISTICS:
LENGTH: 346 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-709-209-217

Query Match 100.0%; Score 793; DB 1; Length 346;
Best Local Similarity 100.0%; Pred. No. 9,1e-87;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
DB 164 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 223

QY 61 CWGELMTLATWGVNLEDPASRDLVVSYNTNMGKFRQLLWPHISCLTFGRETVEIYLV 120
DB 224 CWGELMTLATWGVNLEDPASRDLVVSYNTNMGKFRQLLWPHISCLTFGRETVEIYLV 283

QY 121 SFGWIRTPPAYRPPNAPILSTLPETTV 149
DB 284 SFGWIRTPPAYRPPNAPILSTLPETTV 312

RESULT 9
US-08-458-101-217
Sequence 217, Application US/08458101
Patent No. 5766599
GENERAL INFORMATION:
APPLICANT: Paoletti, Enzo
APPLICANT: Perkus, Marion E.
APPLICANT: Taylor, Jill
APPLICANT: Tartaglia, James
APPLICANT: No. 5766599ton, Elizabeth K.
APPLICANT: Riviere, Michel
APPLICANT: de Taisne, Charles
APPLICANT: Limbach, Keith J.
APPLICANT: Johnson, Gerard P.
APPLICANT: Pincus, Steven E.
APPLICANT: Cox, William I.
APPLICANT: Audonnet, Jean-Christophe Francis
APPLICANT: Gettig, Russell Robert
TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
TITLE OF INVENTION: STRAIN
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford
ADDRESSEE: c/o William S. Frommer
STREET: 530 Fifth Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,101
FILING DATE: 01-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2740

```
TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 217:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 346 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-458-101-217

Query Match 100.0%; Score 793; DB 1; Length 346;
Best Local Similarity 100.0%; Pred. No. 9.1e-87;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
Db 164 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 223

QY 61 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGKFRQLLWFIHISCLTFGRTVIEYLV 120
Db 224 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGKFRQLLWFIHISCLTFGRTVIEYLV 283

QY 121 SFGWIRTPPAYRPPNAPILSTLPETTV 149
Db 284 SFGWIRTPPAYRPPNAPILSTLPETTV 312

RESULT 10
PCT-US96-10602-6
; Sequence 6, Application PC/TUS9610602
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation
; TITLE OF INVENTION: INHIBITION OF HEPATITIS B REPLICATION
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10602
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/017,814
; FILING DATE: 20-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/282001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 397 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-10602-6

Query Match 100.0%; Score 793; DB 5; Length 397;
Best Local Similarity 100.0%; Pred. No. 1.1e-86;
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Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
Db 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60

QY 61 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGKFRQLLWFIHISCLTFGRTVIEYLV 120
Db 61 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGKFRQLLWFIHISCLTFGRTVIEYLV 120

QY 121 SFGWIRTPPAYRPPNAPILSTLPETTV 149
Db 121 SFGWIRTPPAYRPPNAPILSTLPETTV 149

RESULT 11
PCT-US96-10602-12
; Sequence 12, Application PC/TUS9610602
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation
; TITLE OF INVENTION: INHIBITION OF HEPATITIS B REPLICATION
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10602
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/017,814
; FILING DATE: 20-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/282001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 183 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-10602-12

Query Match 99.2%; Score 787; DB 5; Length 183;
Best Local Similarity 99.3%; Pred. No. 2e-86;
Matches 148; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
Db 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60

QY 61 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGKFRQLLWFIHISCLTFGRTVIEYLV 120
Db 61 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGKFRQLLWFIHISCLTFGRTVIEYLV 120

QY 121 SFGWIRTPPAYRPPNAPILSTLPETTV 149
Db 121 SFGWIRTPPAYRPPNAPILSTLPETTV 149
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RESULT 12
PCT-US96-10602-4
; Sequence 4, Application PC/TUS9610602
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation
; TITLE OF INVENTION: INHIBITION OF HEPATITIS B REPLICATION
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10602
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: 60/017,814
; APPLICATION NUMBER: 60/017,814
; FILING DATE: 20-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/282001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 351 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-10602-4

Query Match 99.0%; Score 785; DB 5; Length 351;
Best Local Similarity 98.7%; Pred. No. 8.4e-86;
Matches 147; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALROAIL 60
Db 4 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALROAIL 63

Qy 61 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGKFRQLLWPHISCLTFGRTVIEYLV 120
Db 64 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGKFRQLLWPHISCLTFGRTVIEYLV 123

Qy 121 SFGVWIRTPPAYRPPNAPILSTLPETTV 149
Db 124 SFGVWIRTPPAYRPPNAPILSTLPETTVI 152

RESULT 13
US-08-968-747-20
; Sequence 20, Application US/08968747
; Patent No. 6060595
; GENERAL INFORMATION:
; APPLICANT: Scaglioni et al.
; TITLE OF INVENTION: INHIBITION OF VIRAL REPLICATION
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street

CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/968,747
FILING DATE: 03-SEP-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 08472/705001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 183 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-968-747-20

Query Match 98.1%; Score 778; DB 3; Length 183;
Best Local Similarity 98.7%; Pred. No. 2.4e-85;
Matches 147; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALROAIL 60
Db 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALROAIL 60

Qy 61 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGKFRQLLWPHISCLTFGRTVIEYLV 120
Db 61 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGKFRQLLWPHISCLTFGRTVIEYLV 120

Qy 121 SFGVWIRTPPAYRPPNAPILSTLPETTV 149
Db 121 SFGVWIRTPPAYRPPNAPILSTLPETTV 149

RESULT 14
US-08-968-747-2
; Sequence 2, Application US/08968747
; Patent No. 6060595
; GENERAL INFORMATION:
; APPLICANT: Scaglioni et al.
; TITLE OF INVENTION: INHIBITION OF VIRAL REPLICATION
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/968,747
; FILING DATE: 03-SEP-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.

Matches 145; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDDTASALYREALSPHHTALROAIL 60
DB 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDDTASALYREALSPHHTALROAIL 60
QY 61 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGLKFRQLLWFMHISCLTFGRETVIEYLV 120
DB 61 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGLKFRQLLWFMHISCLTFGRETVIEYLV 120
QY 121 SFGVMIRTPPAYRPPNAPILSTLPETTIV 149
DB 121 SFGVMIRTPPAYRPPNAPILSTLPETTIV 149

Search completed: April 23, 2004, 16:30:53
Job time : 30 secs

REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 08472/705001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 193 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-968-747-2

Query Match 98.1%; Score 778; DB 3; Length 193;
Best Local Similarity 98.7%; Pred. No. 2.5e-85;
Matches 147; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDDTASALYREALSPHHTALROAIL 60
DB 11 MDIDPYKEFGATVELLSFLPSDFPSVRDLDDTASALYREALSPHHTALROAIL 70
QY 61 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGLKFRQLLWFMHISCLTFGRETVIEYLV 120
DB 71 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGLKFRQLLWFMHISCLTFGRETVIEYLV 130
QY 121 SFGVMIRTPPAYRPPNAPILSTLPETTIV 149
DB 131 SFGVMIRTPPAYRPPNAPILSTLPETTIV 159

RESULT 15
US-07-739-642-2
Sequence 2, Application US/07739642
Patent No. 5173427
GENERAL INFORMATION:
APPLICANT: Mallonee, Richard L.
TITLE OF INVENTION: Vectors And Hosts With Increased
TITLE OF INVENTION: Expression Of Hbcag
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard R. Rodrick
STREET: 1 Becton Drive
CITY: Franklin Lakes
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07417-1880
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/739,642
FILING DATE: 19910801
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stierwalt, Brian K.
REGISTRATION NUMBER: 33,213
REFERENCE/DOCKET NUMBER: P-2272
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-848-5317
TELEFAX: 201-848-9228
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
US-07-739-642-2

Query Match 97.7%; Score 775; DB 1; Length 185;
Best Local Similarity 97.3%; Pred. No. 5.5e-85;

GenCore version 5.1.6
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Run on: April 23, 2004, 16:29:45 ; Search time 42 Seconds
(without alignments)
980.829 Million cell updates/sec

Title: US-09-931-325C-170_COPY_1_149
Perfect score: 793
Sequence: 1 MDIDPYKEFGATVLLSFLP.....PAYRPPNAPILSTLPETTV 149

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Gapop 10.0 , Gapext 0.5

Searched: 1133595 seqs, 276475211 residues
Total number of hits satisfying chosen parameters: 1133595

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications AA:*
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 - 2: /cgn2_6/ptodata/2/pubpaa/FCT_NEW_PUB.pep:*
 - 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
 - 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
 - 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
 - 6: /cgn2_6/ptodata/2/pubpaa/FCTUS_PUBCOMB.pep:*
 - 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
 - 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
 - 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
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 - 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
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 - 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
 - 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
 - 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
 - 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	793	100.0	171	10	US-09-930-915A-263
2	793	100.0	183	8	US-08-785-997-38
3	793	100.0	183	10	US-09-387-340-38
4	793	100.0	183	10	US-09-848-616-99
5	793	100.0	183	10	US-09-931-325A-170
6	793	100.0	183	10	US-09-386-591-38
7	793	100.0	183	10	US-09-930-915A-247
8	793	100.0	183	12	US-10-289-456-39
9	793	100.0	183	12	US-10-274-616-1
10	793	100.0	183	14	US-10-243-739-39
11	793	100.0	183	14	US-10-244-065-39
12	793	100.0	183	14	US-10-289-454-39
13	793	100.0	183	14	US-10-050-902-99
14	793	100.0	183	14	US-10-050-898-99
15	793	100.0	183	14	US-10-080-299-1

16	793	100.0	183	14	US-10-082-014-1
17	793	100.0	183	14	US-10-372-076-1
18	793	100.0	183	15	US-10-346-190-39
19	793	100.0	183	15	US-10-465-811-30
20	793	100.0	212	9	US-09-929-955-11
21	793	100.0	212	10	US-09-848-616-114
22	793	100.0	212	12	US-10-289-456-54
23	793	100.0	212	12	US-10-312-045-2
24	793	100.0	212	13	US-10-104-966-11
25	793	100.0	212	14	US-10-243-739-54
26	793	100.0	212	14	US-10-244-065-54
27	793	100.0	212	14	US-10-289-454-54
28	793	100.0	212	14	US-10-050-902-114
29	793	100.0	212	14	US-10-050-898-114
30	793	100.0	212	15	US-10-346-190-54
31	793	100.0	212	15	US-10-465-811-45
32	793	100.0	289	9	US-09-812-862-8
33	793	100.0	397	9	US-09-812-862-6
34	791	99.7	183	10	US-09-848-616-102
35	791	99.7	183	12	US-10-289-456-42
36	791	99.7	183	14	US-10-243-739-42
37	791	99.7	183	14	US-10-244-065-42
38	791	99.7	183	14	US-10-289-454-42
39	791	99.7	183	14	US-10-050-902-102
40	791	99.7	183	14	US-10-050-898-102
41	791	99.7	183	15	US-10-346-190-42
42	791	99.7	183	15	US-10-465-811-33
43	790	99.6	183	10	US-09-848-616-104
44	790	99.6	183	10	US-09-848-616-105
45	790	99.6	183	12	US-10-289-456-44

ALIGNMENTS

RESULT 1
US-09-930-915A-263
; Sequence 263, Application US/09930915A
; Publication No. US20030138765A1
; GENERAL INFORMATION:
; APPLICANT: Birkett, Ashley J.
; TITLE OF INVENTION: IMMUNOGENIC HEC CHIMER PARTICLES HAVING ENHANCED
; FILE REFERENCE: 4564/83501 ICC-102.2 PCT
; CURRENT APPLICATION NUMBER: US/09/930,915A
; CURRENT FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: 60/226,867
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/225,843
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: Patentin ver. 2.1
; SEQ ID NO 263
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-09-930-915A-263

Query Match	100.0%;	Score	793;	DB	10;	Length	171;
Best Local Similarity	100.0%;	Pred. No.	1.3e-80;				
Matches	149;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
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Db	1	MDIDPYKEFGATVLLSFLPSDFPPSVRDLDTASALYREALSPHCSPPHTRQAIL	60				
Qy	61	CWGLMTLATVGVNLEDDPASRLVSVYNTNGLKFRQLLNTHISCLITGRTVIEYLV	120				
Db	61	CWGLMTLATVGVNLEDDPASRLVSVYNTNGLKFRQLLNTHISCLITGRTVIEYLV	120				
Qy	121	SFGVWIRTPPAYRPPNAPILSTLPETTV	149				
Db	121	SFGVWIRTPPAYRPPNAPILSTLPETTV	149				

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Welsh & Katz, Ltd.
;; STREET: 120 South Riverside Plaza, 22nd Floor
;; CITY: Chicago
;; STATE: IL
;; COUNTRY: USA
;; ZIP: 60606
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/387,340
;; FILING DATE:
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Gamson, Edward P.
;; REGISTRATION NUMBER: 29,381
;; REFERENCE/DOCKET NUMBER: MON-102.0 6018/69242
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (312)655-1500
;; TELEFAX: (312)655-1501
;; INFORMATION FOR SEQ ID NO: 38:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 183 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-09-387-340-38
Query Match 100.0%; Score 793; DB 10; Length 183;
Best Local Similarity 100.0%; Pred. No. 1.5e-80;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDIDPYKEFGATVELLSFSPDFFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
DB 1 MDIDPYKEFGATVELLSFSPDFFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
QY 61 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGLKFRQLLWFHISCLTFGRETVEIYLV 120
DB 61 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGLKFRQLLWFHISCLTFGRETVEIYLV 120
QY 121 SFGWIRTPPAYRPPNAPILSTLPTTVV 149
DB 121 SFGWIRTPPAYRPPNAPILSTLPTTVV 149
RESULT 4
US-09-848-616-99
; Sequence 99, Application US/09848616
; Publication No. US20030054010A1
; GENERAL INFORMATION:
; APPLICANT: Sebbel, Peter
; APPLICANT: Dunant, Nicolas
; APPLICANT: Bachmann, Martin
; APPLICANT: Tissot, Alain
; APPLICANT: Lechner, Franziska
; TITLE OF INVENTION: Molecular Antigen Array
; FILE REFERENCE: 1700.0180002
; CURRENT APPLICATION NUMBER: US/09/848,616
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 99
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-09-848-616-99
Query Match 100.0%; Score 793; DB 10; Length 183;
Best Local Similarity 100.0%; Pred. No. 1.5e-80;

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Welsh & Katz, Ltd.
;; STREET: 120 South Riverside Plaza, 22nd Floor
;; CITY: Chicago
;; STATE: IL
;; COUNTRY: USA
;; ZIP: 60606
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/785,997
;; FILING DATE:
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Gamson Ph.D., Edward P.
;; REGISTRATION NUMBER: 29,381
;; REFERENCE/DOCKET NUMBER: MON-101.0 6018/69346
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (312)655-1500
;; TELEFAX: (312)655-1501
;; INFORMATION FOR SEQ ID NO: 38:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 183 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-785-997-38
Query Match 100.0%; Score 793; DB 8; Length 183;
Best Local Similarity 100.0%; Pred. No. 1.5e-80;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MDIDPYKEFGATVELLSFSPDFFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
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DB 61 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGLKFRQLLWFHISCLTFGRETVEIYLV 120
QY 121 SFGWIRTPPAYRPPNAPILSTLPTTVV 149
DB 121 SFGWIRTPPAYRPPNAPILSTLPTTVV 149
RESULT 3
US-09-387-340-38
; Sequence 38, Application US/09387340
; Publication No. US20030026808A1
; GENERAL INFORMATION:
; APPLICANT: Needleman, Philip
; APPLICANT: Glenn, Kevin
; APPLICANT: Krul, Elaine
; APPLICANT: Gamson, Edward P.
; TITLE OF INVENTION: An Immunological Process and Constructs
; FOR INCREASING THE HDL CHOLESTEROL CONCENTRATION
; NUMBER OF SEQUENCES: 50

Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCHSPHHTALRQAIL 60
 Db 1 MDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCHSPHHTALRQAIL 60
 QY 61 CWGELMTLATWGVNLEDPASRDVVSVYNTNMGLKFRQLLWFIHISCLTFGRETVEIYLV 120
 Db 61 CWGELMTLATWGVNLEDPASRDVVSVYNTNMGLKFRQLLWFIHISCLTFGRETVEIYLV 120
 QY 121 SFGWIRTPPAYRPPNAPILSTLPETTV 149
 Db 121 SFGWIRTPPAYRPPNAPILSTLPETTV 149

RESULT 5

US-09-931-325A-170
 ; Sequence 170, Application US/09991325A
 ; Publication No. US20030054337A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Birkett, Ashley J.
 ; TITLE OF INVENTION: VALERIA IMMUNOGEN AND VACCINE
 ; FILE REFERENCE: 4564/83503 ICC-103.1
 ; CURRENT APPLICATION NUMBER: US/09/931.325A
 ; CURRENT FILING DATE: 2002-02-22
 ; PRIOR APPLICATION NUMBER: 60/225,843
 ; PRIOR FILING DATE: 2000-08-16
 ; PRIOR APPLICATION NUMBER: USSN NOT YET ASSIGNED
 ; PRIOR FILING DATE: 2001-08-15
 ; NUMBER OF SEQ ID NOS: 186
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 170
 ; LENGTH: 183
 ; TYPE: PRT
 ; ORGANISM: Hepatitis B virus
 US-09-931-325A-170

Query Match 100.0%; Score 793; DB 10; Length 183;
 Best Local Similarity 100.0%; Pred. No. 1.5e-80;
 Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCHSPHHTALRQAIL 60
 Db 1 MDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCHSPHHTALRQAIL 60
 QY 61 CWGELMTLATWGVNLEDPASRDVVSVYNTNMGLKFRQLLWFIHISCLTFGRETVEIYLV 120
 Db 61 CWGELMTLATWGVNLEDPASRDVVSVYNTNMGLKFRQLLWFIHISCLTFGRETVEIYLV 120
 QY 121 SFGWIRTPPAYRPPNAPILSTLPETTV 149
 Db 121 SFGWIRTPPAYRPPNAPILSTLPETTV 149

RESULT 6

US-09-386-591-38
 ; Sequence 38, Application US/09386591
 ; Publication No. US20030100520A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Needleman, Philip
 ; APPLICANT: Glenn, Kevin
 ; TITLE OF INVENTION: An Immunological Process and Constructs
 ; TITLE OF INVENTION: For Increasing the HDL Cholesterol Concentration by DNA
 ; TITLE OF INVENTION: Vaccination
 ; NUMBER OF SEQUENCES: 52
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Welsh & Katz, Ltd.
 ; STREET: 120 South Riverside Plaza, 22nd Floor
 ; CITY: Chicago
 ; STATE: IL
 ; COUNTRY: USA
 ; ZIP: 60606
 ; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/386,591
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Gamson Ph.D., Edward P.
 REGISTRATION NUMBER: 29,381
 REFERENCE/DOCKET NUMBER: MON-103.0 6221/69656
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312)655-1500
 TELEFAX: (312)655-1501
 INFORMATION FOR SEQ ID NO: 38:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 183 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-386-591-38

Query Match 100.0%; Score 793; DB 10; Length 183;
 Best Local Similarity 100.0%; Pred. No. 1.5e-80;
 Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCHSPHHTALRQAIL 60
 Db 1 MDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCHSPHHTALRQAIL 60
 QY 61 CWGELMTLATWGVNLEDPASRDVVSVYNTNMGLKFRQLLWFIHISCLTFGRETVEIYLV 120
 Db 61 CWGELMTLATWGVNLEDPASRDVVSVYNTNMGLKFRQLLWFIHISCLTFGRETVEIYLV 120
 QY 121 SFGWIRTPPAYRPPNAPILSTLPETTV 149
 Db 121 SFGWIRTPPAYRPPNAPILSTLPETTV 149

RESULT 7

US-09-930-915A-247
 ; Sequence 247, Application US/09930915A
 ; Publication No. US20030138769A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Birkett, Ashley J.
 ; TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES HAVING ENHANCED
 ; TITLE OF INVENTION: STABILITY
 ; FILE REFERENCE: 4564/83501 ICC-102.2 PCT
 ; CURRENT APPLICATION NUMBER: US/09/930,915A
 ; CURRENT FILING DATE: 2001-08-15
 ; PRIOR APPLICATION NUMBER: 60/226,867
 ; PRIOR FILING DATE: 2000-08-22
 ; PRIOR APPLICATION NUMBER: 60/225,843
 ; PRIOR FILING DATE: 2000-08-16
 ; NUMBER OF SEQ ID NOS: 313
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 247
 ; LENGTH: 183
 ; TYPE: PRT
 ; ORGANISM: Hepatitis B virus
 US-09-930-915A-247

Query Match 100.0%; Score 793; DB 10; Length 183;
 Best Local Similarity 100.0%; Pred. No. 1.5e-80;
 Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCHSPHHTALRQAIL 60
 Db 1 MDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCHSPHHTALRQAIL 60
 QY 61 CWGELMTLATWGVNLEDPASRDVVSVYNTNMGLKFRQLLWFIHISCLTFGRETVEIYLV 120

DB 61 CWGELMTLATWGVNLEDPASRDVSVYNTNMGLKFRQLLWPHISCLTFGRETVEIYLV 120
QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVV 149
DB 121 SFGVWIRTPPAYRPPNAPILSTLPETTVV 149
RESULT 8
US-10-289-456-39
; Sequence 39, Application US/10289456
; Publication No. US20040033211A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin
; APPLICANT: Maurer, Patrick
; APPLICANT: Spohn, Gunther
; TITLE OF INVENTION: Antigen Arrays for Treatment of Bone Disease
; FILE REFERENCE: 1700.0330001
; CURRENT APPLICATION NUMBER: US/10/289,456
; CURRENT FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: PCT/IB02/00166
; PRIOR FILING DATE: 2002-01-21
; PRIOR APPLICATION NUMBER: US 10/050,902
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/396,635
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 39
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-10-289-456-39
Query Match 100.0%; Score 793; DB 12; Length 183;
Best Local Similarity 100.0%; Pred. No. 1.5e-80;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
DB 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
QY 61 CWGELMTLATWGVNLEDPASRDVSVYNTNMGLKFRQLLWPHISCLTFGRETVEIYLV 120
DB 61 CWGELMTLATWGVNLEDPASRDVSVYNTNMGLKFRQLLWPHISCLTFGRETVEIYLV 120
QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVV 149
DB 121 SFGVWIRTPPAYRPPNAPILSTLPETTVV 149
RESULT 9
US-10-274-616-1
; Sequence 1, Application US/10274616
; Publication No. US20030202982A1
; GENERAL INFORMATION:
; APPLICANT: Birkett, Ashley J.
; TITLE OF INVENTION: INFLUENZA IMMUNOGEN AND VACCINE
; FILE REFERENCE: ICC 127.0 4564/88545
; CURRENT APPLICATION NUMBER: US/10/274,616
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: 09/930,915
; PRIOR FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: 10/080,299
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Hepatitis B virus

US-10-274-616-1
Query Match 100.0%; Score 793; DB 12; Length 183;
Best Local Similarity 100.0%; Pred. No. 1.5e-80;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
DB 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
QY 61 CWGELMTLATWGVNLEDPASRDVSVYNTNMGLKFRQLLWPHISCLTFGRETVEIYLV 120
DB 61 CWGELMTLATWGVNLEDPASRDVSVYNTNMGLKFRQLLWPHISCLTFGRETVEIYLV 120
QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVV 149
DB 121 SFGVWIRTPPAYRPPNAPILSTLPETTVV 149
RESULT 10
US-10-243-739-39
; Sequence 39, Application US/10243739
; Publication No. US20030091593A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F.
; APPLICANT: Storni, Tazio
; APPLICANT: Lechner, Franziska
; TITLE OF INVENTION: In vivo Activation of Antigen Presenting Cells for Enhancement of
; TITLE OF INVENTION: Immune Responses Induced by Virus Like Particles
; FILE REFERENCE: 1700.0210001
; CURRENT APPLICATION NUMBER: US/10/243,739
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 60/318,967
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 39
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-10-243-739-39
Query Match 100.0%; Score 793; DB 14; Length 183;
Best Local Similarity 100.0%; Pred. No. 1.5e-80;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
DB 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
QY 61 CWGELMTLATWGVNLEDPASRDVSVYNTNMGLKFRQLLWPHISCLTFGRETVEIYLV 120
DB 61 CWGELMTLATWGVNLEDPASRDVSVYNTNMGLKFRQLLWPHISCLTFGRETVEIYLV 120
QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVV 149
DB 121 SFGVWIRTPPAYRPPNAPILSTLPETTVV 149
RESULT 11
US-10-244-065-39
; Sequence 39, Application US/10244065
; Publication No. US20030099668A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F.
; APPLICANT: Storni, Tazio
; APPLICANT: Maurer, Patrick
; APPLICANT: Tissot, Alain
; APPLICANT: Schwarz, Katrin
; APPLICANT: Meijerink, Edwin
; APPLICANT: Lipowsky, Gerard
; APPLICANT: Pumpens, Paul
; APPLICANT: Cielens, Indulis

```
; APPLICANT: Renhofa, Regina
; TITLE OF INVENTION: Packaging of Immunostimulatory Substances into Virus-like Particles
; FILE REFERENCE: 1700.0220001
; CURRENT APPLICATION NUMBER: US/10/244,065
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 60/374,145
; PRIOR FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: 60/318,994
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 39
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-10-244-065-39

Query Match      100.0%; Score 793; DB 14; Length 183;
Best Local Similarity 100.0%; Pred. No. 1.5e-80;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
DB 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
QY 61 CWGELMTLATWGVNLEDPASRDVLVSYVNTNMGLKFRQLLWFWHISCLTFTGRETVEIYLV 120
DB 61 CWGELMTLATWGVNLEDPASRDVLVSYVNTNMGLKFRQLLWFWHISCLTFTGRETVEIYLV 120
QY 121 SFGWIRTPPAYRPPNAPILSTLPETTV 149
DB 121 SFGWIRTPPAYRPPNAPILSTLPETTV 149

RESULT 12
US-10-289-454-39
; Sequence 39, Application US/10289454
; Publication No. US20030157479A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin
; APPLICANT: Jennings, Gary
; APPLICANT: Sonderegger, Ivo
; TITLE OF INVENTION: Antigen Arrays for Treatments of Allergic Eosinophilic Diseases
; FILE REFERENCE: 1700.0360001
; CURRENT APPLICATION NUMBER: US/10/289,454
; CURRENT FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: US 60/396,636
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: PCT/IB02/00166
; PRIOR FILING DATE: 2002-01-21
; PRIOR APPLICATION NUMBER: US 10/050,902
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 386
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 39
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-10-289-454-39

Query Match      100.0%; Score 793; DB 14; Length 183;
Best Local Similarity 100.0%; Pred. No. 1.5e-80;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
DB 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
QY 61 CWGELMTLATWGVNLEDPASRDVLVSYVNTNMGLKFRQLLWFWHISCLTFTGRETVEIYLV 120
DB 61 CWGELMTLATWGVNLEDPASRDVLVSYVNTNMGLKFRQLLWFWHISCLTFTGRETVEIYLV 120
QY 121 SFGWIRTPPAYRPPNAPILSTLPETTV 149
DB 121 SFGWIRTPPAYRPPNAPILSTLPETTV 149

RESULT 14
US-10-050-898-99
; Sequence 99, Application US/10050898
; Publication No. US20030175711A1
; GENERAL INFORMATION:
; APPLICANT: Renner, Wolfgang A.
; APPLICANT: Bachmann, Martin
; APPLICANT: Tissot, Alain
; APPLICANT: Maurer, Patrick
; APPLICANT: Lechner, Franziska
; APPLICANT: Sebbel, Peter
; APPLICANT: Piessek, Christine
; APPLICANT: Ortmann, Rainer
; APPLICANT: Luond, Rainer
; APPLICANT: Staufenbiel, Matthias
; APPLICANT: Frey, Peter
; TITLE OF INVENTION: Molecular Antigen Array
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Search completed: April 23, 2004, 16:35:28
Job time : 43 secs

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FILE REFERENCE: 1700.0190005
CURRENT APPLICATION NUMBER: US/10/050,898
CURRENT FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US 60/262,379
PRIOR FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: US 60/288,549
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/326,998
PRIOR FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: US 60/331,045
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 350
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 99
LENGTH: 183
TYPE: PRT
ORGANISM: Hepatitis B virus
US-10-050-898-99
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Query Match 100.0%; Score 793; DB 14; Length 183;
Best Local Similarity 100.0%; Pred. No. 1.5e-80;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
Db 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60

Qy 61 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGLKFRQLLWFHISCLTFGRETVIEYLV 120
Db 61 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGLKFRQLLWFHISCLTFGRETVIEYLV 120

Qy 121 SFGWIRTPPAYRPPNAPILSTLPETTV 149
Db 121 SFGWIRTPPAYRPPNAPILSTLPETTV 149
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RESULT 15
US-10-080-299-1
Sequence 1, Application US/10080299
Publication No. US20030175863A1
GENERAL INFORMATION:
APPLICANT: Birkett, Ashley J.
TITLE OF INVENTION: INFLUENZA IMMUNOGEN AND VACCINE
FILE REFERENCE: ICC 127.0 4564/84273
CURRENT APPLICATION NUMBER: US/10/080,299
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 09/930,915
PRIOR FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 83
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 183
TYPE: PRT
ORGANISM: Hepatitis B virus
US-10-080-299-1
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Query Match 100.0%; Score 793; DB 14; Length 183;
Best Local Similarity 100.0%; Pred. No. 1.5e-80;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
Db 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60

Qy 61 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGLKFRQLLWFHISCLTFGRETVIEYLV 120
Db 61 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGLKFRQLLWFHISCLTFGRETVIEYLV 120

Qy 121 SFGWIRTPPAYRPPNAPILSTLPETTV 149
Db 121 SFGWIRTPPAYRPPNAPILSTLPETTV 149
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OM protein - protein search, using sw model

Run on: April 23, 2004, 16:26:09 ; Search time 20 Seconds
(without alignments)
716.627 Million cell updates/sec

Title: US-09-931-325C-170_COPY_1_149
Perfect score: 793
Sequence: 1 MDIDPYKEGATVLLSFLP.....PAYRPPNAPILSLPETTVV 149

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:.*
1: PIR1:.*
2: PIR2:.*
3: PIR3:.*
4: PIR4:.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	793	100.0	212	1	NKVLAAH	e antigen precursor
2	790	99.6	212	2	S53211	e antigen precursor
3	790	99.6	212	2	S32204	e antigen precursor
4	790	99.6	212	2	S20750	e antigen precursor
5	790	99.6	212	2	S53200	e antigen precursor
6	788	99.4	212	2	S53216	e antigen precursor
7	788	99.4	212	2	S53272	e antigen precursor
8	788	99.4	212	2	S53281	e antigen precursor
9	787	99.2	183	2	S53270	core antigen - hep
10	787	99.2	212	2	S53225	e antigen precursor
11	787	99.2	212	2	S53274	e antigen precursor
12	787	99.2	212	2	S53163	core antigen - hep
13	786	99.1	183	2	S53169	core antigen - hep
14	784	98.9	183	2	S53247	core antigen - hep
15	784	98.9	212	2	S53251	e antigen precursor
16	784	98.9	212	2	S20746	e antigen precursor
17	783	98.7	212	2	S53202	e antigen precursor
18	783	98.7	212	2	S53204	e antigen precursor
19	782	98.6	183	2	S53260	core antigen - hep
20	782	98.6	212	2	S53198	e antigen precursor
21	781	98.5	212	2	S53129	core antigen - hep
22	781	98.5	212	2	S53223	e antigen precursor
23	781	98.5	212	2	S53227	e antigen precursor
24	779	98.2	183	2	S53240	core antigen - hep
25	778	98.1	212	2	S53253	core antigen - hep
26	776	97.9	183	2	S53152	core antigen - hep
27	776	97.9	212	1	NKVLHH	e antigen precursor
28	776	97.9	212	2	S53240	e antigen precursor
29	775	97.7	212	2	S53240	e antigen precursor

RESULT 1

NKVLAAH
e antigen precursor / core antigen - hepatitis B virus (subtype ayw4, isolate hb321 and N;Alternate names: HBe antigen precursor / HBe antigen; pre-C/C antigen
N;Contains: core antigen; e antigen
C;Species: hepatitis B virus, HBV
A;Variety: subtype ayw4, isolate hb321; isolate patient Ferracuti'83; isolate patient Ca cheri'83
C;Date: 18-Dec-1981 #sequence revision 08-Nov-1996 #text change 16-Jul-1999
C;Accession: S47405; S53191; S53209; S53234; S53264; S53249; S53262; S53277; A03711
R;Plucieniczak, A.
A;Description: Molecular cloning and sequencing of two complete genomes of polish isolat
A;Reference number: S47404
A;Accession: S47405
A;Molecule type: DNA
A;Residues: 1-212 <PLU>
A;Cross-references: EMBL:Z35716; NID:G527435; PIDN:CAA84786.1; PID:G527437
A;Experimental source: subtype ayw4, isolate hb321
R;Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
submitted to the EMBL Data Library, March 1995
A;Reference number: S53112
A;Accession: S53191
A;Molecule type: DNA
A;Residues: 1-212 <LA1>
A;Cross-references: EMBL:X85283; NID:G736088; PIDN:CAA59593.1; PID:G736090
A;Experimental source: isolate patient Ferracuti'83
A;Accession: S53209
A;Molecule type: DNA
A;Residues: 1-212 <LA2>
A;Cross-references: EMBL:X85290; NID:G736114; PIDN:CAA59609.1; PID:G736116
A;Experimental source: isolate patient Casteg'83
A;Accession: S53234
A;Molecule type: DNA
A;Residues: 1-212 <LA3>
A;Cross-references: EMBL:X85300; NID:G736150; PIDN:CAA59631.1; PID:G736152
A;Experimental source: isolate patient Sanna'84
A;Accession: S53264
A;Molecule type: DNA
A;Residues: 1-212 <LA4>
A;Cross-references: EMBL:X85313; NID:G736194; PIDN:CAA59659.1; PID:G736196
A;Experimental source: isolate patient Licheri-1'85
A;Accession: S53249
A;Molecule type: DNA
A;Residues: 1-212 <LA5>
A;Cross-references: EMBL:X85306; NID:G736172; PIDN:CAA59644.1; PID:G736174
A;Experimental source: isolate patient Flore-1'86
A;Accession: S53262
A;Molecule type: DNA
A;Residues: 1-212 <LA6>
A;Cross-references: EMBL:X85312; NID:G736191; PIDN:CAA59657.1; PID:G736193
A;Experimental source: isolate patient Licheri'83

ALIGNMENTS

A:Accession: S53277
 A:Molecule type: DNA
 A:Residues: 30-212 <LAI>
 A:Cross-references: EMBL:X85317; NID:G736211; PIDN:CAA59669.1; PID:G736214
 A:Experimental source: patient Giordano-2/86
 A:Note: due to a stop codon between the e antigen precursor
 R;Galibert, F.; Mandart, E.; Fitoussi, F.; Tiollais, P.; Charnay, P.
 Nature 281, 646-650, 1979
 A:Title: Nucleotide sequence of the hepatitis B virus genome (subtype ayw) in E. coli.
 A:Reference number: A93214; MUID:81012091; PMID:399327
 A:Accession: A03711
 A:Molecule type: DNA
 A:Residues: 1-212 <GAL>
 A:Cross-references: GB:J02203; NID:G329640; PIDN:AAA45489.1; PID:G329642
 A:Experimental source: subtype ayw
 C:Genetics:
 A:Gene: C
 C:Superfamily: hepatitis B virus core antigen
 C:Keywords: alternative initiators; core protein
 F:1-29/Domain: signal sequence #status predicted <SIG>
 F:30-212/Product: core antigen #status predicted <CAG>
 F:179-212/Domain: carboxyl-terminal propeptide #link EAG #status predicted <BCP>
 Query Match 100.0%; Score 793; DB 1; Length 212;
 Best Local Similarity 100.0%; Pred. No. 2.4e-72;
 Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDIDPKFEGATVLLSFLPSDFPVSVDLDTASALYREALSPHCSPHHTALRQAIL 60
 DB 30 MDIDPKFEGATVLLSFLPSDFPVSVDLDTASALYREALSPHCSPHHTALRQAIL 89
 QY 61 CWGELMTLATWGVNLEDPASDLVSVYNTNMGKFRQLLWPHISCLTFGRTVIEYLV 120
 DB 90 CWGELMTLATWGVNLEDPASDLVSVYNTNMGKFRQLLWPHISCLTFGRTVIEYLV 149
 QY 121 SFGWIRTPPAYRPPNAPILSTLPETTV 149
 DB 150 SFGWIRTPPAYRPPNAPILSTLPETTV 178
 RESULT 2
 S53211
 e antigen precursor / core antigen - hepatitis B virus (isolate patient Castag-1'85 and
 N;Alternate names: HBC antigen; HBe antigen precursor / HBe antigen; pre-C/C antigen
 C:Species: hepatitis B virus, HBV
 C:Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 26-Aug-1999
 C:Accession: S53211; S53197
 R;Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
 submitted to the EMBL Data Library, March 1995
 A:Reference number: S53112
 A:Accession: S53211
 A:Molecule type: DNA
 A:Residues: 1-212 <LAI>
 A:Cross-references: EMBL:X85291; NID:G736117; PIDN:CAA59611.1; PID:G736119
 A:Experimental source: isolate patient Castag-1'85
 A:Accession: S53197
 A:Molecule type: DNA
 A:Residues: 30-212 <LAW>
 A:Cross-references: EMBL:X85284; NID:G736095; PIDN:CAA59596.1; PID:G736098
 A:Experimental source: isolate patient Ferracuti-1'89
 A:Note: due to a stop codon between the alternative initiators the e antigen precursor
 C:Genetics:
 A:Gene: C
 C:Superfamily: hepatitis B virus core antigen
 C:Keywords: alternative initiators; core protein
 F:1-29/Domain: signal sequence #status predicted <SIG>
 F:30-212/Product: core antigen #status predicted <CAG>
 F:179-212/Domain: carboxyl-terminal propeptide #link EAG #status predicted <BCP>

Query Match 99.6%; Score 790; DB 2; Length 212;
 Best Local Similarity 99.3%; Pred. No. 4.9e-72;
 Matches 148; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDIDPKFEGATVLLSFLPSDFPVSVDLDTASALYREALSPHCSPHHTALRQAIL 60
 DB 30 MDIDPKFEGATVLLSFLPSDFPVSVDLDTASALYREALSPHCSPHHTALRQAIL 89
 QY 61 CWGELMTLATWGVNLEDPASDLVSVYNTNMGKFRQLLWPHISCLTFGRTVIEYLV 120
 DB 90 CWGELMTLATWGVNLEDPASDLVSVYNTNMGKFRQLLWPHISCLTFGRTVIEYLV 149
 QY 121 SFGWIRTPPAYRPPNAPILSTLPETTV 149
 DB 150 SFGWIRTPPAYRPPNAPILSTLPETTV 178
 RESULT 3
 S32204
 e antigen precursor / core antigen - hepatitis B virus (subtype ayw, patients C1000 and
 N;Alternate names: HBe antigen precursor / HBe antigen; pre-C/C antigen
 C:Species: hepatitis B virus, HBV
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Oct-2000
 C:Accession: S32204; S53207
 R;Preisler-Adams, S.; Schlayer, M.J.; Peters, T.; Hettler, F.; Rasenack, J.
 submitted to the EMBL Data Library, March 1993
 A:Description: Identification and sequence analysis of hepatitis B virus DNA in immunologic
 A:Reference number: S32202
 A:Accession: S32204
 A:Molecule type: DNA
 A:Residues: 1-212 <PRE>
 A:Cross-references: EMBL:X72702; NID:G288927; PIDN:CAA51257.1; PID:G288930
 A:Experimental source: subtype ayw, patient C1000
 R;Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
 submitted to the EMBL Data Library, March 1995
 A:Reference number: S53112
 A:Accession: S53207
 A:Molecule type: DNA
 A:Residues: 30-212 <LAI>
 A:Cross-references: EMBL:X85289; NID:G736110; PIDN:CAA59607.1; PID:G736113
 A:Experimental source: isolate patient Castag-2'87
 A:Note: due to a stop codon mutation between the alternative initiators the e antigen f
 C:Genetics:
 A:Gene: C
 C:Superfamily: hepatitis B virus core antigen
 C:Keywords: alternative initiators; core protein
 F:1-29/Domain: signal sequence #status predicted <SIG>
 F:30-212/Product: core antigen #status predicted <CAG>
 F:179-212/Domain: carboxyl-terminal propeptide #link EAG #status predicted <BCP>
 Query Match 99.6%; Score 790; DB 2; Length 212;
 Best Local Similarity 99.3%; Pred. No. 4.9e-72;
 Matches 148; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDIDPKFEGATVLLSFLPSDFPVSVDLDTASALYREALSPHCSPHHTALRQAIL 60
 DB 30 MDIDPKFEGATVLLSFLPSDFPVSVDLDTASALYREALSPHCSPHHTALRQAIL 89
 QY 61 CWGELMTLATWGVNLEDPASDLVSVYNTNMGKFRQLLWPHISCLTFGRTVIEYLV 120
 DB 90 CWGELMTLATWGVNLEDPASDLVSVYNTNMGKFRQLLWPHISCLTFGRTVIEYLV 149
 QY 121 SFGWIRTPPAYRPPNAPILSTLPETTV 149
 DB 150 SFGWIRTPPAYRPPNAPILSTLPETTV 178
 RESULT 4
 S20750
 e antigen precursor / core antigen - hepatitis B virus (subtype ayw, patient CI)
 N;Alternate names: HBe antigen precursor / HBe antigen; pre-C/C antigen

N:Contains: core antigen; e antigen
 C:Species: hepatitis B virus, HBV
 A:Variety: subtype ayw, patient CI
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
 C:Accession: S20750
 R:Lai, M.E.; Mazzoleni, A.P.; Balestrieri, A.; Porru, A.
 submitted to the EMBL Data Library, March 1995
 A:Description: Sequence analysis of HBV genomes isolated from patients with HBSAg negative
 A:Reference number: S20745
 A:Accession: S20750
 A:Molecule type: DNA
 A:Residues: 1-212 <LAI>
 A:Cross-references: EMBL:X65258; NID:G59434; PIDN:CAA46354.1; PID:G59436
 A:Experimental source: subtype ayw, patient CI
 C:Genetics:
 A:Gene: C
 C:Superfamily: hepatitis B virus core antigen
 C:Keywords: alternative initiators; core protein
 F:1-29/Domain: signal sequence #status predicted <SIG>
 F:30-212/Product: core antigen #status predicted <CAG>
 F:30-178/Product: e antigen #status predicted <EAG>
 F:179-212/Domain: carboxyl-terminal propeptide #link EAG #status predicted <ECP>

Query Match 99.6%; Score 790; DB 2; Length 212;
 Best Local Similarity 99.3%; Pred. No. 4.9e-72;
 Matches 148; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIDPKFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
 DB 30 MDIDPKFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 89

QY 61 CWGELMTLATWGVNLEDPASRDLVVSYVNTNMGKFLQLLWFHISCLTFGRETVEYLV 120
 DB 90 CWGELMTLATWGVNLEDPASRDLVVSYVNTNMGKFLQLLWFHISCLTFGRETVEYLV 149

QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVV 149
 DB 150 SFGVWIRTPPAYRPPNAPILSTLPETTVV 178

RESULT 5
 S53200
 e antigen precursor / core antigen - hepatitis B virus (isolate patient Ferracuti-3'91)
 N:Alternate names: HBe antigen precursor / HBC antigen; pre-C/C antigen
 N:Contains: core antigen; e antigen
 C:Species: hepatitis B virus, HBV
 A:Variety: isolate patient Ferracuti-3'91
 C:Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 26-Aug-1999
 C:Accession: S53200
 R:Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
 submitted to the EMBL Data Library, March 1995
 A:Reference number: S53112
 A:Accession: S53200
 A:Molecule type: DNA
 A:Residues: 1-212 <LAI>
 A:Cross-references: EMBL:X85286; NID:G736101; PIDN:CAA59600.1; PID:G736103
 A:Experimental source: isolate patient Ferracuti-3'91
 C:Genetics:
 A:Gene: C
 C:Superfamily: hepatitis B virus core antigen
 C:Keywords: alternative initiators; core protein
 F:1-29/Domain: signal sequence #status predicted <SIG>
 F:30-212/Product: core antigen #status predicted <CAG>
 F:30-178/Product: e antigen #status predicted <EAG>
 F:179-212/Domain: carboxyl-terminal propeptide #link EAG #status predicted <ECP>

Query Match 99.6%; Score 790; DB 2; Length 212;
 Best Local Similarity 99.3%; Pred. No. 4.9e-72;
 Matches 148; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIDPKFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
 DB 30 MDIDPKFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 89

QY 61 CWGELMTLATWGVNLEDPASRDLVVSYVNTNMGKFLQLLWFHISCLTFGRETVEYLV 120
 DB 90 CWGELMTLATWGVNLEDPASRDLVVSYVNTNMGKFLQLLWFHISCLTFGRETVEYLV 149

QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVV 149
 DB 150 SFGVWIRTPPAYRPPNAPILSTLPETTVV 178

RESULT 6
 S53216
 e antigen precursor / core antigen - hepatitis B virus (isolate patient Castag'3)
 N:Alternate names: HBe antigen precursor / HBC antigen; pre-C/C antigen
 N:Contains: core antigen; e antigen
 C:Species: hepatitis B virus, HBV
 A:Variety: isolate patient Castag'3
 C:Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 26-Aug-1999
 C:Accession: S53216
 R:Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
 submitted to the EMBL Data Library, March 1995
 A:Reference number: S53112
 A:Accession: S53216
 A:Molecule type: DNA
 A:Residues: 1-212 <LAI>
 A:Cross-references: EMBL:X85293; NID:G736124; PIDN:CAA59616.1; PID:G736126
 A:Experimental source: isolate patient Castag'3
 C:Genetics:
 A:Gene: C
 C:Superfamily: hepatitis B virus core antigen
 C:Keywords: alternative initiators; core protein
 F:1-29/Domain: signal sequence #status predicted <SIG>
 F:30-212/Product: core antigen #status predicted <CAG>
 F:30-178/Product: e antigen #status predicted <EAG>
 F:179-212/Domain: carboxyl-terminal propeptide #link EAG #status predicted <ECP>

Query Match 99.4%; Score 788; DB 2; Length 212;
 Best Local Similarity 99.3%; Pred. No. 7.7e-72;
 Matches 148; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDIDPKFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
 DB 30 MDIDPKFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 89

QY 61 CWGELMTLATWGVNLEDPASRDLVVSYVNTNMGKFLQLLWFHISCLTFGRETVEYLV 120
 DB 90 CWGELMTLATWGVNLEDPASRDLVVSYVNTNMGKFLQLLWFHISCLTFGRETVEYLV 149

QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVV 149
 DB 150 SFGVWIRTPPAYRPPNAPILSTLPETTVV 178

RESULT 7
 S53272
 e antigen precursor / core antigen - hepatitis B virus (isolate patient Licheri-3'90)
 N:Alternate names: HBe antigen precursor / HBC antigen; pre-C/C antigen
 N:Contains: core antigen; e antigen
 C:Species: hepatitis B virus, HBV
 A:Variety: isolate patient Licheri-3'90
 C:Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 26-Aug-1999
 C:Accession: S53272
 R:Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
 submitted to the EMBL Data Library, March 1995
 A:Reference number: S53112
 A:Accession: S53272
 A:Molecule type: DNA
 A:Residues: 1-212 <LAI>
 A:Cross-references: EMBL:X85315; NID:G736205; PIDN:CAA59664.1; PID:G736207
 A:Experimental source: isolate patient Licheri-3'90
 C:Genetics:
 A:Gene: C
 C:Superfamily: hepatitis B virus core antigen

Query Match 99.6%; Score 790; DB 2; Length 212;
 Best Local Similarity 99.3%; Pred. No. 4.9e-72;
 Matches 148; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIDPKFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
 DB 30 MDIDPKFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 89

C;Keywords: alternative initiators; core protein
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-212/Product: core antigen #status predicted <CAG>
F;30-178/Product: e antigen #status predicted <EAG>
F;179-212/Domain: carboxyl-terminal propeptide #link EAG #status predicted <ECP>

Query Match 99.4%; Score 788; DB 2; Length 212;
Best Local Similarity 99.3%; Pred. No. 7,7e-72;
Matches 148; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVELLSFLPSDFPVSVDLLDTASALYREALSPHCSPHHTALRQAIL 60
DB 30 MDIDPYKEFGATVELLSFLPSDFPVSVDLLDTASALYREALSPHCSPHHTALRQAIL 89
QY 61 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGKFRQLLWPHISCLTFGRETVEIYLV 120
DB 90 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGKFRQLLWPHISCLTFGRETVEIYLV 149
QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVV 149
DB 150 SFGVWIRTPPAYRPPNAPILSTLPETTVV 178

RESULT 8
S53281
e antigen precursor / core antigen - hepatitis B virus (isolate patient Galistru-1'86)
N;Alternate names: HBe antigen precursor / HBeC antigen; pre-C/C antigen
N;Contains: core antigen; e antigen
C;Species: hepatitis B virus, HBV
A;Variety: isolate patient Galistru-1'86
C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 26-Aug-1999
R;Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
submitted to the EMBL Data Library, March 1995
A;Accession: S53281
A;Molecule type: DNA
A;Residues: 1-212 <LAI>
A;Cross-references: EMBL:X85319; NID:g736218; PIDN:CAAS9673.1; PID:g736220
A;Experimental source: isolate patient Galistru-1'86
C;Genetics:
A;Gene: C
C;Superfamily: hepatitis B virus core antigen
C;Keywords: alternative initiators; core protein
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-212/Product: core antigen #status predicted <CAG>
F;30-178/Product: e antigen #status predicted <EAG>
F;179-212/Domain: carboxyl-terminal propeptide #link EAG #status predicted <ECP>

Query Match 99.4%; Score 788; DB 2; Length 212;
Best Local Similarity 99.3%; Pred. No. 7,7e-72;
Matches 148; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVELLSFLPSDFPVSVDLLDTASALYREALSPHCSPHHTALRQAIL 60
DB 30 MDIDPYKEFGATVELLSFLPSDFPVSVDLLDTASALYREALSPHCSPHHTALRQAIL 89
QY 61 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGKFRQLLWPHISCLTFGRETVEIYLV 120
DB 90 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGKFRQLLWPHISCLTFGRETVEIYLV 149
QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVV 149
DB 150 SFGVWIRTPPAYRPPNAPILSTLPETTVV 178

RESULT 9
S53270
core antigen - hepatitis B virus (isolate patient Licheri-2'87)
N;Alternate names: HBeC antigen
N;Contains: core antigen
C;Species: hepatitis B virus, HBV
A;Variety: isolate patient Licheri-2'87

C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 26-Aug-1999
C;Accession: S53270
R;Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
submitted to the EMBL Data Library, March 1995
A;Reference number: S53112
A;Accession: S53270
A;Molecule type: DNA
A;Residues: 1-183 <LAI>
A;Cross-references: EMBL:X85314; NID:g736201; PIDN:CAAS9662.1; PID:g736204
A;Experimental source: isolate patient Licheri-2'87
A;Note: due to a stop codon between the alternative initiators the e antigen precursor
C;Genetics:
A;Gene: C
C;Superfamily: hepatitis B virus core antigen
C;Keywords: core protein

Query Match 99.2%; Score 787; DB 2; Length 183;
Best Local Similarity 98.7%; Pred. No. 8,2e-72;
Matches 147; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVELLSFLPSDFPVSVDLLDTASALYREALSPHCSPHHTALRQAIL 60
DB 1 MDIDPYKEFGATVELLSFLPSDFPVSVDLLDTASALYREALSPHCSPHHTALRQAIL 60
QY 61 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGKFRQLLWPHISCLTFGRETVEIYLV 120
DB 61 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGKFRQLLWPHISCLTFGRETVEIYLV 120
QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVV 149
DB 121 SFGVWIRTPPAYRPPNAPILSTLPETTVV 149

RESULT 10
S53225
e antigen precursor / core antigen - hepatitis B virus (isolate patient Chighine-2'86)
N;Alternate names: HBe antigen precursor / HBeC antigen; pre-C/C antigen
N;Contains: core antigen; e antigen
C;Species: hepatitis B virus, HBV
A;Variety: isolate patient Chighine-2'86
C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 26-Aug-1999
C;Accession: S53225
R;Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
submitted to the EMBL Data Library, March 1995
A;Reference number: S53112
A;Accession: S53225
A;Molecule type: DNA
A;Residues: 1-212 <LAI>
A;Cross-references: EMBL:X85296; NID:g736137; PIDN:CAAS9622.1; PID:g736139
A;Experimental source: isolate patient Chighine-2'86
C;Genetics:
A;Gene: C
C;Superfamily: hepatitis B virus core antigen
C;Keywords: alternative initiators; core protein
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-212/Product: core antigen #status predicted <CAG>
F;30-178/Product: e antigen #status predicted <EAG>
F;179-212/Domain: carboxyl-terminal propeptide #link EAG #status predicted <ECP>

Query Match 99.2%; Score 787; DB 2; Length 212;
Best Local Similarity 98.7%; Pred. No. 9,8e-72;
Matches 147; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVELLSFLPSDFPVSVDLLDTASALYREALSPHCSPHHTALRQAIL 60
DB 30 MDIDPYKEFGATVELLSFLPSDFPVSVDLLDTASALYREALSPHCSPHHTALRQAIL 89
QY 61 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGKFRQLLWPHISCLTFGRETVEIYLV 120
DB 90 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGKFRQLLWPHISCLTFGRETVEIYLV 149
QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVV 149

Db 150 SFGVWIRTPPAYRPPNAPILSTLPETTV 178

RESULT 11

S53274
e antigen precursor / core antigen - hepatitis B virus (isolate patient Giordo'84)
N/Alternate names: HBe antigen precursor / Hbc antigen; pre-C/C antigen
N/Contains: core antigen; e antigen
C/Species: hepatitis B virus, HBV
A/Variety: isolate patient Giordo'84

C/Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 26-Aug-1999

C/Accession: S53274

R/Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.

submitted to the EMBL Data Library, March 1995

A/Reference number: S53112

A/Accession: S53274

A/Molecule type: DNA

A/Residues: 1-212 <LAI>

A/Cross-references: EMBL:X85316; NID:g736208; PIDN:CAA59666.1; PID:g736210

A/Experimental source: isolate patient Giordo'84

C/Genetics:

A/Gene: C

C/Superfamily: hepatitis B virus core antigen

C/Keywords: alternative initiators; core protein

F/1-29/Domain: signal sequence #status predicted <SIG>

F/30-212/Product: core antigen #status predicted <CAG>

F/30-178/Product: e antigen #status predicted <EAG>

F/179-212/Domain: carboxyl-terminal propeptide #link EAG #status predicted <ECP>

Query Match 99.2%; Score 787; DB 2; Length 212;

Best Local Similarity 99.3%; Pred. No. 9.8e-72;

Matches 148; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MDIDPYKEFGATVLLSFLPSDFPSPVRDLDTASALYREALSPHCHSPHHTALRQAIL 60

Db 30 MDIDPYKEFGATVLLSFLPSDFPSPVRDLDTASALYREALSPHCHSPHHTALRQAIL 89

Qy 61 CWGELMTLATWGVNLEDPASRDLYVSVYNTNMGLKFRQLLWFHISCLTFGRETVEIYLV 120

Db 90 CWGELMTLATWGVNLEDPASRDLYVSVYNTNMGLKFRQLLWFHISCLTFGRETVEIYLV 149

Qy 121 SFGVWIRTPPAYRPPNAPILSTLPETTV 149

Db 150 SFGVWIRTPPAYRPPNAPILSTLPETTV 178

RESULT 12

S53163

e antigen precursor / core antigen - hepatitis B virus (isolate patient Vittorina'92)

N/Alternate names: HBe antigen precursor / Hbc antigen; pre-C/C antigen

N/Contains: core antigen; e antigen

C/Species: hepatitis B virus, HBV

A/Variety: isolate patient Vittorina'92

C/Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 26-Aug-1999

C/Accession: S53163

R/Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.

submitted to the EMBL Data Library, March 1995

A/Reference number: S53112

A/Accession: S53163

A/Molecule type: DNA

A/Residues: 1-212 <LAI>

A/Cross-references: EMBL:X85256; NID:g736050; PIDN:CAA59519.1; PID:g736052

A/Experimental source: isolate patient Vittorina'92

C/Genetics:

A/Gene: C

C/Superfamily: hepatitis B virus core antigen

C/Keywords: alternative initiators; core protein

F/1-29/Domain: signal sequence #status predicted <SIG>

F/30-212/Product: core antigen #status predicted <CAG>

F/30-178/Product: e antigen #status predicted <EAG>

F/179-212/Domain: carboxyl-terminal propeptide #link EAG #status predicted <ECP>

Query Match

99.2%; Score 787; DB 2; Length 212;

Best Local Similarity 99.3%; Pred. No. 9.8e-72;
Matches 148; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MDIDPYKEFGATVLLSFLPSDFPSPVRDLDTASALYREALSPHCHSPHHTALRQAIL 60

Db 30 MDIDPYKEFGATVLLSFLPSDFPSPVRDLDTASALYREALSPHCHSPHHTALRQAIL 89

Qy 61 CWGELMTLATWGVNLEDPASRDLYVSVYNTNMGLKFRQLLWFHISCLTFGRETVEIYLV 120

Db 90 CWGELMTLATWGVNLEDPASRDLYVSVYNTNMGLKFRQLLWFHISCLTFGRETVEIYLV 149

Qy 121 SFGVWIRTPPAYRPPNAPILSTLPETTV 149

Db 150 SFGVWIRTPPAYRPPNAPILSTLPETTV 178

RESULT 13

S53169

core antigen - hepatitis B virus (isolate patient Muresu'89)

N/Alternate names: HBC antigen

N/Contains: core antigen

C/Species: hepatitis B virus, HBV

A/Variety: isolate patient Muresu'89

C/Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 26-Aug-1999

C/Accession: S53169

R/Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.

submitted to the EMBL Data Library, March 1995

A/Reference number: S53112

A/Accession: S53169

A/Molecule type: DNA

A/Residues: 1-183 <LAI>

A/Cross-references: EMBL:X85275; NID:g736057; PIDN:CAA59571.1; PID:g736060

A/Experimental source: isolate patient Muresu'89

A/Note: due to a stop codon between the alternative initiators the e antigen precursor

C/Genetics:

A/Gene: C

C/Superfamily: hepatitis B virus core antigen

C/Keywords: core protein

Query Match 99.1%; Score 786; DB 2; Length 183;

Best Local Similarity 98.7%; Pred. No. 1e-71;

Matches 147; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MDIDPYKEFGATVLLSFLPSDFPSPVRDLDTASALYREALSPHCHSPHHTALRQAIL 60

Db 1 MDIDPYKEFGATVLLSFLPSDFPSPVRDLDTASALYREALSPHCHSPHHTALRQAIL 60

Qy 61 CWGELMTLATWGVNLEDPASRDLYVSVYNTNMGLKFRQLLWFHISCLTFGRETVEIYLV 120

Db 61 CWGELMTLATWGVNLEDPASRDLYVSVYNTNMGLKFRQLLWFHISCLTFGRETVEIYLV 120

Qy 121 SFGVWIRTPPAYRPPNAPILSTLPETTV 149

Db 121 SFGVWIRTPPAYRPPNAPILSTLPETTV 149

RESULT 14

S53247

core antigen - hepatitis B virus (isolate patient Flore-2'91)

N/Alternate names: HBC antigen

N/Contains: core antigen

C/Species: hepatitis B virus, HBV

A/Variety: isolate patient Flore-2'91

C/Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 26-Aug-1999

C/Accession: S53247

R/Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.

submitted to the EMBL Data Library, March 1995

A/Reference number: S53112

A/Accession: S53247

A/Molecule type: DNA

A/Residues: 1-183 <LAI>

A/Cross-references: EMBL:X85305; NID:g736168; PIDN:CAA59642.1; PID:g736171

A/Experimental source: isolate patient Flore-2'91

A>Note: due to a stop codon between the alternative initiators the e antigen precursor
C:Genetics:
A:Gene: C
C:Superfamily: hepatitis B virus core antigen
C:Keywords: core protein

Query Match 98.9%; Score 784; DB 2; Length 183;
Best Local Similarity 98.7%; Pred. No. 1.6e-71; Mismatches 1; Indels 0; Gaps 0;
Matches 147; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MDIDPYKEGATVELLSFLPSDFPVSRLDLDTSALYREALSPHCSPHHTALRQAIL 60
Db 1 MDIDPYKEGATVELLSFLPSDFPVSRLDLDTSALYREALSPHCSPHHTALRQAIL 60
QY 61 CWGELMTLATWGVNLEDPASRLDVSVYNTNMGLKFRQLLWPHISCLTFGRETVEIYLV 120
Db 61 CWGELMTLATWGVNLEDPASRLDVSVYNTNMGLKFRQLLWPHISCLTFGRETVEIYLV 120
QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTV 149
Db 121 SFGVWIRTPPAYRPPNAPILSTLPETCVV 149

RESULT 15

S53251
e antigen precursor / core antigen - hepatitis B virus (isolate patient Flore'85)
N;Alternate names: HBe antigen precursor / HBe antigen; pre-C/C antigen
N;Contains: core antigen; e antigen
C;Species: hepatitis B virus, HBV
A;Variety: isolate patient Flore'85
C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 26-Aug-1999
C;Accession: S53251
R;Jai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
submitted to the EMBL Data Library, March 1995
A;Reference number: S53112
A;Accession: S53251
A;Molecule type: DNA
A;Residues: 1-212 <LAI>
A;Cross-references: EMBL:X85307; NID:g736175; PIDN:CAAS9646.1; PID:g736177
A;Experimental source: isolate patient Flore'85
C:Genetics:
A:Gene: C
C:Superfamily: hepatitis B virus core antigen
C:Keywords: alternative initiators; core protein
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-212/Product: core antigen #status predicted <CAG>
F;30-178/Product: e antigen #status predicted <EAG>
F;179-212/Domain: carboxyl-terminal propeptide #link EAG #status predicted <ECP>

Query Match 98.9%; Score 784; DB 2; Length 212;
Best Local Similarity 98.7%; Pred. No. 2e-71; Mismatches 1; Indels 0; Gaps 0;
Matches 147; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MDIDPYKEGATVELLSFLPSDFPVSRLDLDTSALYREALSPHCSPHHTALRQAIL 60
Db 30 MDIDPYKEGATVELLSFLPSDFPVSRLDLDTSALYREALSPHCSPHHTALRQAIL 89
QY 61 CWGELMTLATWGVNLEDPASRLDVSVYNTNMGLKFRQLLWPHISCLTFGRETVEIYLV 120
Db 90 CWGDLTTLATWGVNLEDPASRLDVSVYNTNMGLKFRQLLWPHISCLTFGRETVEIYLV 149
QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTV 149
Db 150 SFGVWIRTPPAYRPPNAPILSTLPETTV 178

Search completed: April 23, 2004, 16:30:16
Job time : 26 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 23, 2004, 16:22:09 ; Search time 18 Seconds
(without alignments)
431.025 Million cell updates/sec

Title: US-09-931-325C-170_COPY_1_149
Perfect score: 793
Sequence: 1 MDIDPKYKFGATVLLSFLP.....PAYRPPNAPILSTLPETTVV 149

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues
Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	793	100.0	183	1	CORA_HPBVY
2	774	97.6	183	1	CORA_HPBVZ
3	772	97.4	185	1	CORA_HPBVM
4	772	97.4	211	1	CORA_HPBVA
5	771	97.2	185	1	CORA_HPBV2
6	761	96.0	183	1	CORA_HPBVU
7	761	96.0	183	1	CORA_HPBVO
8	760	95.8	183	1	CORA_HPBV4
9	756	95.3	214	1	CORA_HPBV9
10	754	95.1	183	1	CORA_HPBVL
11	751	94.7	183	1	CORA_HPBVT
12	749	94.5	195	1	CORA_HPBVF
13	538	67.8	188	1	CORA_HBV1
14	534.5	67.4	217	1	CORA_HPBGS
15	529	66.7	187	1	CORA_HVH8
16	132	16.6	305	1	CORA_HPBH8
17	112	14.1	305	1	CORA_HPBDB
18	112	14.1	305	1	CORA_HPBDC
19	112	14.1	305	1	CORA_HPBDM
20	110	13.9	305	1	CORA_HPBDM
21	85	10.7	306	1	RM45_MOUSE
22	79.5	10.0	3695	1	LM45_HUMAN
23	78	9.8	802	1	BCB2_ACEXY
24	76.5	9.6	1226	1	YE41_METUA
25	75.5	9.5	3148	1	HD_FUGRU
26	75	9.5	784	1	DPQ2_AERPE
27	74	9.3	540	1	HXTD_YEAST
28	73.5	9.3	3587	1	SRF2_BACSU
29	73	9.2	1657	1	IQG1_HUMAN
30	72.5	9.1	306	1	RM45_HUMAN
31	72.5	9.1	2415	1	SPCA_MOUSE
32	72	9.1	377	1	YILO_YEAST
33	72	9.1	455	1	HSJU_XANAC

ALIGNMENTS

RESULT 1

ID	CORA_HPBVY	STANDARD;	PRT;	183 AA.
AC	P03146;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Core antigen.			
GN	C			
OS	Hepatitis B virus (subtype ayw).			
OC	Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.			
OX	NCBI_TaxID=10418;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=8102091; PubMed=399327;			
RA	Galibert F., Mandart E., Fickoussi F., Tiollais P., Charnay P.;			
RT	"Nucleotide sequence of the hepatitis B virus genome (subtype ayw)			
RT	Cloned in E. coli."			
RL	Nature 281:646-650(1979).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=latvia;			
RX	MEDLINE=85204337; PubMed=3996597;			
RA	Bichko V., Fushko P., Dreilina D., Pumpen P., Gren E.;			
RT	"Subtype ayw variant of hepatitis B virus. DNA primary structure			
RT	analysis."			
RL	FEBS Lett. 185:208-212(1985).			
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CC	-----			
DR	EMBL; V01460; CAA34706.1; ALT INIT.			
DR	EMBL; X02496; -; NOT ANNOTATED_CDS.			
DR	InterPro; IPR002006; Hepatitis core.			
DR	Pfam; PF00906; Hepatitis core; 1.			
FT	Core protein; Repeat.			
FT	REPEAT 162 169			
FT	REPEAT 170 177			
FT	VARIANT 33 33			
FT	VARIANT 80 80			
FT	SEQUENCE 183 AA; E0D9D9763F24E958 CRC64;			
SQ	-----			
Query Match	100.0%;	Score 793;	DB 1;	Length 183;
Best Local Similarity	100.0%;	Pred. No. 1.8e-72;		
Matches 149;	Conservative 0;	Mismatches 0;	Gaps 0;	

Qy	1	MDIDPKYKFGATVLLSFLPDPFPPSVRLDPTASALYREALESPHCSPHHTALRQAIL	60
Db	1	MDIDPKYKFGATVLLSFLPDPFPPSVRLDPTASALYREALESPHCSPHHTALRQAIL	60
Qy	61	CWCELTMTATWGVNLEDPAERDLVSVYNTNMGKFLQMLFWHISCLATFGRETVEYLV	120

006596 mycobacteri
Q19978 caenorhabdi
P58050 arabidopsis
Q9Y210 homo sapien
P09917 homo sapien
Q01738 phanerochaet
P36304 kenedya ye
P34833 caenorhabdi
P58565 anabaena sp
Q03287 escherichia
Q06206 proteus mir
Q9Zde9 rickettsia

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Db 61 CWGELMTLATWGVNLEDPASRDVSVYNTNMGKFRQLLWFHISCLTGTRETVIEYLV 120
QY 121 SFGWIRTPPAYRPPNAPILSTLPTTVV 149
Db 121 SFGWIRTPPAYRPPNAPILSTLPTTVV 149

RESULT 2
CORA HPBVZ
ID CORA HPBVZ STANDARD; PRT; 183 AA.
AC P03147;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-OCT-1989 (Rel. 12, Last annotation update)
DE Core antigen.
GN C.
OS Hepatitis B virus (subtype ady).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10419;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8102115; PubMed=39329;
RA Pask M., Goto T., Gilbert W., Zink B., Schaller H., McKay P.,
RA Leadbetter G., Murray K.;
RT "Hepatitis B virus genes and their expression in E. coli.";
RL Nature 282:575-579(1979).
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CC EMBL; J02202; AAA45486.1; -
CC DR EMBL; A08967; CAA00816.1; -
CC DR PIR; B93217; NKVL2.
CC DR InterPro; IPR002006; Hepatitis_core.
CC DR Pfam; PF00906; Hepatitis_core; 1.
CC DR Core protein; Repeat.
CC KW REPEAT 162 169
CC FT REPEAT 170 177
CC SQ SEQUENCE 183 AA; 21042 MW; 545ED0E5527F26C CRC64;

Query Match 97.6%; Score 774; DB 1; Length 183;
Best Local Similarity 96.0%; Pred. No. 1.5e-70;
Matches 143; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
Db 1 MDIDPYKEFGATVLLSFLPSDFPSVRDLDTAAALYREALSPHCSPHHTALRQAIL 60
QY 61 CWGELMTLATWGVNLEDPASRDVSVYNTNMGKFRQLLWFHISCLTGTRETVIEYLV 120
Db 61 CWGELMTLATWGVNLEDPASRDVSVYNTNMGKFRQLLWFHISCLTGTRETVIEYLV 120
QY 61 CWGELMTLATWGVNLEDPASRDVSVYNTNMGKFRQLLWFHISCLTGTRETVIEYLV 120
Db 61 CWGELMTLATWGVNLEDPASRDVSVYNTNMGKFRQLLWFHISCLTGTRETVIEYLV 120
QY 121 SFGWIRTPPAYRPPNAPILSTLPTTVV 149
Db 121 SFGWIRTPPAYRPPNAPILSTLPTTVV 149

RESULT 3
CORA HPBVW
ID CORA HPBVW STANDARD; PRT; 185 AA.
AC P03149;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-OCT-1989 (Rel. 12, Last annotation update)
DE Core antigen.
GN C.
OS Hepatitis B virus (subtype adw).
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OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=106821;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83168919; PubMed=6300776;
RA Ono Y., Onda H., Sasada R., Igarashi K., Sugino Y., Nishioka K.;
RT "The complete nucleotide sequences of the cloned hepatitis B virus
RT DNA; subtype adr and adw.";
RL Nucleic Acids Res. 11:1747-1757(1983).
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CC EMBL; V00866; -; NOT_ANNOTATED_CDS.
CC DR InterPro; IPR002006; Hepatitis_core.
CC DR Pfam; PF00906; Hepatitis_core; 1.
CC DR Core protein; Repeat.
CC KW REPEAT 164 171
CC FT REPEAT 172 179
CC SQ SEQUENCE 185 AA; 21394 MW; B86A90D541BA70F9 CRC64;

Query Match 97.4%; Score 772; DB 1; Length 185;
Best Local Similarity 96.6%; Pred. No. 2.3e-70;
Matches 144; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
Db 1 MDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
QY 61 CWGELMTLATWGVNLEDPASRDVSVYNTNMGKFRQLLWFHISCLTGTRETVIEYLV 120
Db 61 CWGELMTLATWGVNLEDPASRDVSVYNTNMGKFRQLLWFHISCLTGTRETVIEYLV 120
QY 121 SFGWIRTPPAYRPPNAPILSTLPTTVV 149
Db 121 SFGWIRTPPAYRPPNAPILSTLPTTVV 149

RESULT 4
CORA HPBYA
ID CORA HPBYA STANDARD; PRT; 211 AA.
AC P24023;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Core antigen.
GN C.
OS Hepatitis B virus (strain alphas).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10411;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90266476; PubMed=2345966;
RA Tong S., Li J., Vitvitski L., Trepo C.;
RT "Active hepatitis B virus replication in the presence of anti-HBe is
RT associated with viral variants containing an inactive pre-C region.";
RL Virology 176:596-603(1990).
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CC
CC EMBL; M32138; -; NOT_ANNOTATED_CDS.
CC DR PIR; A34773; NKVL1.
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DR InterPro: IPR002006; Hepatitis core.
DR Pfam: PF00906; Hepatitis_core_1.
KW Core protein; Repeat.
FT REPEAT 183 190
FT REPEAT 198 206
SQ SEQUENCE 211 AA; 24208 MW; B774AC72E65C75AB CRC64;

Query Match 97.4%; Score 772; DB 1; Length 211;
Best Local Similarity 96.6%; Pred. No. 2.7e-70;
Matches 144; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVLLSFLSPDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
DB 29 MDIDPYKEFGATVLLSFLSPDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 88
QY 61 CWGELMTLATWGVNLEDPASRDVSVYNTNMGKFRQLLWPHISCLTFGRVIEYLV 120
DB 89 CWGLITLSTWGVNLEDPASRDVSVYNTNMGKFRQLLWPHISCLTFGRVIEYLV 148
QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTV 149
DB 149 SFGVWIRTPPAYRPPNAPILSTLPETTV 177

RESULT 5
CORA HPBV2
ID CORA HPBV2 STANDARD; PRT; 185 AA.
AC P03148;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Core antigen.
OS Hepatitis B virus (subtype adw2).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10408;
RN [1]
RP SEQUENCE FROM N.A.
RA Valenzuela P., Quiroga M., Zaldivar J., Gray P., Rutter W.J.;
RL (in) Field B.N., Jaenisch R., Fox C.F. (eds.);
RL Animal virus genetics, pp.57-70, Academic Press, New York (1980).
DR InterPro: IPR002006; Hepatitis_core.
DR Pfam: PF00906; Hepatitis_core; 1.
KW Core protein; Repeat.
FT REPEAT 164 171
FT REPEAT 172 179
SQ SEQUENCE 185 AA; 21304 MW; 31F4DC338B507E19 CRC64;

Query Match 97.2%; Score 771; DB 1; Length 185;
Best Local Similarity 96.6%; Pred. No. 2.9e-70;
Matches 144; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVLLSFLSPDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
DB 1 MDIDPYKEFGATVLLSFLSPDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
QY 61 CWGELMTLATWGVNLEDPASRDVSVYNTNMGKFRQLLWPHISCLTFGRVIEYLV 120
DB 61 CWGELMTLATWGVNLEDPASRDVSVYNTNMGKFRQLLWPHISCLTFGRVIEYLV 120
QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTV 149
DB 121 SFGVWIRTPPAYRPPNAPILSTLPETTV 149

RESULT 6
CORA HPBVJ
ID CORA HPBVJ STANDARD; PRT; 183 AA.
AC P17391;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Core antigen.

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OS Hepatitis B virus (subtype adw / strain Japan/pJ2W233).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10413;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89010694; PubMed=3171552;
RA Okamoto H., Tsuda F., Sakugawa H., Sastrosowigno R.I., Imai M.,
RA Miyakawa Y., Mayumi M.;
RT "Typing hepatitis B virus by homology in nucleotide sequence:
RT comparison of surface antigen subtypes.";
RL J. Gen. Virol. 69:2575-2583(1988).
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CC EMBL; D00329; -; NOT_ANNOTATED_CDS.
DR PIR; A28925; NKVLJ1.
DR InterPro: IPR002006; Hepatitis_core.
DR Pfam: PF00906; Hepatitis_core; 1.
KW Core protein; Repeat.
FT REPEAT 162 169
FT REPEAT 170 177
SQ SEQUENCE 183 AA; 21224 MW; 9FDD6B5F5AF5E160 CRC64;

Query Match 96.0%; Score 761; DB 1; Length 183;
Best Local Similarity 95.3%; Pred. No. 2.9e-69;
Matches 142; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVLLSFLSPDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
DB 1 MDIDPYKEFGATVLLSFLSPDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
QY 61 CWGELMTLATWGVNLEDPASRDVSVYNTNMGKFRQLLWPHISCLTFGRVIEYLV 120
DB 61 CWGELMTLATWGVNLEDPASRDVSVYNTNMGKFRQLLWPHISCLTFGRVIEYLV 120
QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTV 149
DB 121 SFGVWIRTPPAYRPPNAPILSTLPETTV 149

RESULT 7
CORA HPBVO
ID CORA HPBVO STANDARD; PRT; 183 AA.
AC P17392;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Core antigen.
OS Hepatitis B virus (subtype adw / strain Okinawa/pODW282).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10415;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89010694; PubMed=3171552;
RA Okamoto H., Tsuda F., Sakugawa H., Sastrosowigno R.I., Imai M.,
RA Miyakawa Y., Mayumi M.;
RT "Typing hepatitis B virus by homology in nucleotide sequence:
RT comparison of surface antigen subtypes.";
RL J. Gen. Virol. 69:2575-2583(1988).
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CC -----
DR EMBL; D00330; -, NOT ANNOTATED_CDS.
DR PIR; B28925; NKVLJ2.
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
KW Core protein; Repeat.
FT REPEAT 162 169
FT REPEAT 170 177
SQ SEQUENCE 183 AA; 668DB2633122930C CRC64;

Query Match 96.0%; Score 761; DB 1; Length 183;
Best Local Similarity 95.3%; Pred. No. 2.9e-69;
Matches 142; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDIDPKYKFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
Db 1 MDIDPKYKFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
QY 61 CWGELMTLATWGVNLEDPASRLDVSYVNTNMGKFRQLLWFIHISCLTFGRETVEIYLV 120
Db 61 CWGELMTLATWGVNLEDPASRLDVSYVNTNMGKFRQLLWFIHISCLTFGRETVEIYLV 120
QY 121 SFGWIRTPPAYRPPNAPILSTLPETTV 149
Db 121 SFGWIRTPPAYRPPNAPILSTLPETTV 149

RESULT 8
COR_A_HPBV4 STANDARD; PRT; 193 AA.
ID COR_A_HPBV4
AC P03150; P03151;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Core antigen.
DE Core antigen.
GN Hepatitis B virus (subtype adr4), and
OS Hepatitis B virus (subtype adr), and
OS Hepatitis B virus (subtype adr / strain Indonesia/pIDW420).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
CK NCBI_TaxID=10409, 106820, 10412;
RN [1]
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ADR;
RX MEDLINE=831168919; PubMed=6300776;
RA Ono Y., Onda H., Sasada R., Igarashi K., Sugino Y., Nishioka K.;
RT "The complete nucleotide sequences of the cloned hepatitis B virus
RT DNA; subtype adr and adr.";
RL Nucleic Acids Res. 11:1747-1757(1983).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ADR4;
RX MEDLINE=83246570; PubMed=6306594;
RA Fujiyama A., Miyazonara A., Nozaki C., Yoneyama T., Ohtomo N.,
RA Matsubara K.;
RT "Cloning and structural analyses of hepatitis B virus DNAs, subtype
RT adr.";
RL Nucleic Acids Res. 11:4601-4610(1983).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=ADW;
RX MEDLINE=89010694; PubMed=3171552;
RA Okamoto H., Tsuda F., Sakugawa H., Sastrosoewignjo R.I., Imai M.,
RA Miyakawa Y., Mayumi M.;
RT "Typing hepatitis B virus by homology in nucleotide sequence:
RT comparison of surface antigen subtypes.";
RL J. Gen. Virol. 69:2575-2583(1988).
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CC -----
DR EMBL; X51970; CAA36232.1; -
DR PIR; S10381; NKVLKS.
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
KW Core protein; Repeat.
FT REPEAT 193 200
FT REPEAT 201 208
SQ SEQUENCE 214 AA; 24722 MW; 2D668333EC5AFB8C CRC64;

Query Match 95.3%; Score 756; DB 1; Length 214;
Best Local Similarity 96.0%; Pred. No. 1.1e-66;
Matches 143; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDIDPKYKFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
Db 30 MDIDPKYKFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 89
QY 61 CWGELMTLATWGVNLEDPASRLDVSYVNTNMGKFRQLLWFIHISCLTFGRETVEIYLV 120
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CC -----
DR EMBL; X01587; CAA25745.1; -
DR PIR; D00331; -, NOT ANNOTATED_CDS.
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
KW Core protein; Repeat.
FT REPEAT 162 169
FT REPEAT 170 177
SQ SEQUENCE 183 AA; 21095 MW; ED2DA1DB07F596D CRC64;

Query Match 95.8%; Score 760; DB 1; Length 183;
Best Local Similarity 94.6%; Pred. No. 3.7e-69;
Matches 141; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDIDPKYKFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
Db 1 MDIDPKYKFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
QY 61 CWGELMTLATWGVNLEDPASRLDVSYVNTNMGKFRQLLWFIHISCLTFGRETVEIYLV 120
Db 61 CWGELMTLATWGVNLEDPASRLDVSYVNTNMGKFRQLLWFIHISCLTFGRETVEIYLV 120
QY 121 SFGWIRTPPAYRPPNAPILSTLPETTV 149
Db 121 SFGWIRTPPAYRPPNAPILSTLPETTV 149

RESULT 9
COR_A_HPBV9 STANDARD; PRT; 214 AA.
ID COR_A_HPBV9
AC P17039;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE Core antigen.
DE Core antigen.
GN Hepatitis B virus (subtype adr / strain 991).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
CK NCBI_TaxID=10410;
RN [1]
RN [2]
RP SEQUENCE FROM N.A.
RC Koechel H.G., Schueler A., Lottmann S., Thomssen R.;
RX Submitted (FEB-1990) to the EMBL/GenBank/DBJ databases.
RL -----
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CC -----
DR EMBL; X51970; CAA36232.1; -
DR PIR; S10381; NKVLKS.
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
KW Core protein; Repeat.
FT REPEAT 193 200
FT REPEAT 201 208
SQ SEQUENCE 214 AA; 24722 MW; 2D668333EC5AFB8C CRC64;

Query Match 95.3%; Score 756; DB 1; Length 214;
Best Local Similarity 96.0%; Pred. No. 1.1e-66;
Matches 143; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDIDPKYKFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
Db 30 MDIDPKYKFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 89
QY 61 CWGELMTLATWGVNLEDPASRLDVSYVNTNMGKFRQLLWFIHISCLTFGRETVEIYLV 120
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Db 90 CWGELMTLATVWGNLDPASRDVNVYNTNMGKIRQLLWFRISVLTFGRETIVLEYLV 149
Qy 121 SFGVWIRTPPAYRPPNAPILSTLPETTV 149
Db 150 SFGVWIRTPPAYRPPNAPILSTLPETTV 178

RESULT 10
CORA_HPBVL STANDARD; PRT; 183 AA.
AC P12901;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Core antigen.
GN C.
OS Hepatitis B virus (strain lsh / chimpanzee isolate).
OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10414;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88258473; PubMed=2838576;
RA Vaudin M., Wolstenholme A.J., Tsiquaye K.N., Zuckerman A.J.,
RA Harrison T.J.;
RT "The complete nucleotide sequence of the genome of a hepatitis B
RT virus isolated from a naturally infected chimpanzee."
RL J. Gen. Virol. 69:1383-1389(1988).
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CC -----
DR EMBL; D00220; BAA00157.1; -
DR PIR; A28885; NKVLCR.
DR PDB; 1HHH; 31-OCT-93.
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
KW Core protein; Repeat; 3D-structure.
FT REPEAT 162 169
FT REPEAT 170 177
SQ SEQUENCE 183 AA; 20999 MW; 923DCB94A33FC0B8 CRC64;

Query Match 95.1%; Score 754; DB 1; Length 183;
Best Local Similarity 94.6%; Pred. No. 1.5e-68;
Matches 141; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MDIDPYKEFGATVVELLSFLPSDFPSVRDLDTASALYREALSPHCHSPHTALRQAIL 60
Db 1 MDIDPYKEFGATVVELLSFLPSDFPSVRDLDTASALYREALSPHCHSPHTALRQAIL 60
Qy 61 CWGELMTLATVWGNLDPASRDVNVYNTNMGKIRQLLWFRISVLTFGRETIVLEYLV 120
Db 61 CWGELMTLATVWGNLDPASRDVNVYNTNMGKIRQLLWFRISVLTFGRETIVLEYLV 120

RESULT 11
CORA_HPBVT STANDARD; PRT; 212 AA.
AC Q05495;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Core antigen.
GN C.
OS Hepatitis B virus (subtyp adw2 variant sf).
OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=31515;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90169850; PubMed=2307406;
RA Bhat R.A., Ulrich P.P., Vyas G.N.;
RT "Molecular characterization of a new variant of hepatitis B virus in
RT a persistently infected homosexual man."
RL Hepatology 11:271-276(1990).
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
KW Core protein; Repeat.
FT REPEAT 174 181
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OS Hepatitis B virus (subtyp adw4 / strain Brazil / isolate w4B).
OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=45410;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93346970; PubMed=8345355;
RA Naumann H., Schaefer S., Yoshida C.F.T., Gaspar A.M.C., Repp R.,
RA Gerlich W.H.;
RT "Identification of a new hepatitis B virus (HBV) genotype from Brazil
RT that expresses HBV surface antigen subtype adw4."
RL J. Gen. Virol. 74:1627-1632(1993).
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CC -----
DR EMBL; X69798; CAA49452.1; -
DR PIR; JQ2227; JQ2227.
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
KW Core protein; Repeat.
FT DOMAIN 178 204 ARG-RICH. 3 X 5 AA REPEATS OF S-P-R-R-R.
FT DOMAIN 184 203
FT REPEAT 184 188 1.
FT REPEAT 191 195 2.
FT REPEAT 199 203 3.
FT REPEAT 212 AA; 24234 MW; F832610DB7C36FD2 CRC64;
SQ SEQUENCE 212 AA; 24234 MW; F832610DB7C36FD2 CRC64;

Query Match 94.7%; Score 751; DB 1; Length 212;
Best Local Similarity 93.3%; Pred. No. 3.5e-68;
Matches 139; Conservative 8; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MDIDPYKEFGATVVELLSFLPSDFPSVRDLDTASALYREALSPHCHSPHTALRQAIL 60
Db 30 MDIDPYKEFGATVVELLSFLPSDFPSVRDLDTASALYREALSPHCHSPHTALRQAIL 89
Qy 61 CWGELMTLATVWGNLDPASRDVNVYNTNMGKIRQLLWFRISVLTFGRETIVLEYLV 120
Db 90 CWGELMTLATVWGNLDPASRDVNVYNTNMGKIRQLLWFRISVLTFGRETIVLEYLV 149
Qy 121 SFGVWIRTPPAYRPPNAPILSTLPETTV 149
Db 150 SFGVWIRTPPAYRPPNAPILSTLPETTV 178

RESULT 12
CORA_HPBVF STANDARD; PRT; 195 AA.
AC P29178;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE Core antigen.
GN C.
OS Hepatitis B virus (subtyp adw2 variant sf).
OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=31515;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90169850; PubMed=2307406;
RA Bhat R.A., Ulrich P.P., Vyas G.N.;
RT "Molecular characterization of a new variant of hepatitis B virus in
RT a persistently infected homosexual man."
RL Hepatology 11:271-276(1990).
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
KW Core protein; Repeat.
FT REPEAT 174 181
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FT REPEAT 182 189
SQ SEQUENCE 195 AA; 22461 MW; E2B166F879CB7CB7 CRC64;

Query Match 94.5%; Score 749; DB 1; Length 195;
Best Local Similarity 94.0%; Pred. No. 5e-68;
Matches 140; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVLLSPDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
DB 13 LDIDPYKEFGATVLLSPDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 72
QY 61 CWGELMTLATVGNLEDPASRDLVVSYVNTNMGLKFRQLLWPHISCLTFGRETVEYLV 120
DB 73 CWVELMTLATVGNLEDPASRDLVVSYVNTNMGLKFRQLLWPHISCLTFGRETVEYLV 132
QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTV 149
DB 133 SFGVWIRTPPAYRPPNAPILSTLPETTV 161

RESULT 13
CORA WHV1 STANDARD; PRT; 188 AA.
AC P03152;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Core antigen.
GN C.
OS Woodchuck hepatitis virus 1 (WHV 1),
OS Woodchuck hepatitis virus 7 (WHV 7),
OS Woodchuck hepatitis virus 59 (WHV 59), and
OS Woodchuck hepatitis virus 8 (infectious clone) (WHV 8).
OC Viruses; Retroviruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10430, 10432, 10431, 10434;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=Woodchuck hepatitis virus 1;
RX MEDLINE=82216969; PubMed=7086958;
RA Galibert F., Chen T.N., Mandart E.;
RE "Nucleotide sequence of a cloned woodchuck hepatitis virus genome: comparison with the hepatitis B virus sequence.";
RT J. Virol. 41:51-65(1982).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=Woodchuck hepatitis virus 7, and Woodchuck hepatitis virus 59;
RX MEDLINE=88101359; PubMed=3336938;
RA Cohen J.I., Miller R.H., Rosenblum B., Denniston K., Gerin J.L., Purcell R.H.;
RE "Sequence comparison of woodchuck hepatitis virus replicative forms shows conservation of the genome.";
RT Virology 162:12-20(1988).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=Woodchuck hepatitis virus 8 (infectious clone);
RX MEDLINE=89184524; PubMed=2928306;
RA Girones R., Cote P.J., Hornbuckle W.E., Tennant B.C., Gerin J.L., Purcell R.H., Miller R.H.;
RE "Complete nucleotide sequence of a molecular clone of woodchuck hepatitis virus that is infectious in the natural host.";
RT Proc. Natl. Acad. Sci. U.S.A. 86:1846-1849(1989).
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CC EMBL; J02442; AAA46761.1;
CC EMBL; M18753; AAA46769.1;
CC EMBL; M19183; AAA46765.1;

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DR EMBL; J04514; AAA46772.1;
DR PIR; C32397; NKVLC.
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
KW Core protein; Repeat.
FT REPEAT 167 174
FT REPEAT 175 182
SQ SEQUENCE 188 AA; 21693 MW; 1F4454D0A7B7CE42 CRC64;

Query Match 67.8%; Score 538; DB 1; Length 188;
Best Local Similarity 64.4%; Pred. No. 7.2e-47;
Matches 96; Conservative 20; Mismatches 33; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVLLSPDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
DB 1 MDIDPYKEFGATVLLSPDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
QY 61 CWGELMTLATVGNLEDPASRDLVVSYVNTNMGLKFRQLLWPHISCLTFGRETVEYLV 120
DB 61 CWDELTKLIANSSNITSEQVTIIVNVNDTWGLKVRQSLWFLHSLCTFGHTQVEFLV 120
QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTV 149
DB 121 SFGVWIRTPPAYRPPNAPILSTLPETTV 149

RESULT 14
CORA HPBGs STANDARD; PRT; 217 AA.
AC P03153;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-JAN-1990 (Rel. 13, Last annotation update)
DE Core antigen.
GN C.
OS Ground squirrel hepatitis virus (GSV).
OC Viruses; Retroviruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10406;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84267998; PubMed=6086950;
RA Seeger C., Ganem D., Varmus H.E.;
RE "Nucleotide sequence of an infectious molecularly cloned genome of ground squirrel hepatitis virus.";
RT J. Virol. 51:367-375(1984).
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CC
CC EMBL; K02715; AAA46755.1;
CC PIR; A03715; NKVLS.
CC InterPro; IPR002006; Hepatitis_core.
CC Pfam; PF00906; Hepatitis_core; 1.
KW Core protein; Repeat.
FT REPEAT 196 203
FT REPEAT 204 211
SQ SEQUENCE 217 AA; 25189 MW; DF489467355EC11A CRC64;

Query Match 67.4%; Score 534.5; DB 1; Length 217;
Best Local Similarity 65.1%; Pred. No. 1.9e-46;
Matches 97; Conservative 19; Mismatches 32; Indels 1; Gaps 1;

QY 1 MDIDPYKEFGATVLLSPDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
DB 31 MDIDPYKEFGATVLLSPDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 90
QY 61 CWGELMTLATVGNLEDPASRDLVVSYVNTNMGLKFRQLLWPHISCLTFGRETVEYLV 120

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Db 91 CWEELTRLITWMSNTTEVRR-IIVDHVNNTWGLKVRQTLWEHLSCLTGQHTVQEFV 149
Qy 121 SFGVWIRTPPAYRPPNAPILSTLPEHTV 149
Db 150 SFGVWIRTPPAYRPPNAPILSTLPEHTV 178

RESULT 15

CORA WHV8 STANDARD; PRT; 187 AA.
AC P06433;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 01-OCT-1989 (Rel. 12, Last annotation update)
DE Core antigen.
DE C
GN Woodchuck hepatitis virus 8 (WHV 8).
OS Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
OC NCBI_TaxID=10433;
OX [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=86062931; PubMed=3855246;
RA Kodama K., Ogasawara N., Yoshikawa H., Murakami S.;
RT "Nucleotide sequence of a cloned woodchuck hepatitis virus genome:
RT evolutionary relationship between hepadnaviruses.";
RL J. Virol. 56:978-986(1985).
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CC -----
CC EMBL: M11082; AAA19185.1; -
DR PIR: A03714; NKVLC2.
DR InterPro: IPR002006; Hepatitis core.
DR Pfam: PF00906; Hepatitis_core; 1.
DR Core protein; Repeat.
FT REPEAT 166 173
FT REPEAT 174 181
SQ SEQUENCE 187 AA; 21579 MW; D4BC446FF7163165 CRC64;

Query Match 66.7%; Score 529; DB 1; Length 187;
Best Local Similarity 63.8%; Pred.No. 5.7e-46;
Matches 95; Conservative 20; Mismatches 34; Indels 0; Gaps 0;
Qy 1 MDIDPYKEFGATVELLGLPSPDFPSVRDLDTASALYREALSPHCSPHHTALQAIL 60
Db 1 MDIDPYKEFGSSYQLNPLFLDFPDNLAVDTATLYBELTGTREHCSPHHTALQALV 60
Qy 61 CWGELMTLATWGVNLEDPASRDVLVSYVNTNMGLKFRQLLWPHISCLTGTRETVEYLV 120
Db 61 CWDELTKLIAMSSNITSEQVRTIIVNHVNDTWGLKVRQSLWPHLSCLTGTQHTVQEFV 120
Qy 121 SFGVWIRTPPAYRPPNAPILSTLPEHTV 149
Db 121 SFVWVIRTPPAYRPPNAPILSTLPEHTV 149

Search completed: April 23, 2004, 16:28:46
Job time : 19 secs

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OM protein - protein search, using sw model

Run on: April 23, 2004, 16:25:39 ; Search time 39 Seconds
(without alignments)
1205.441 Million cell updates/sec

Title: US-09-931-325C-170_COPY_1_149
Perfect score: 793
Sequence: 1 MDIDPYKEFGATVELLSFLP.....PAYRPPNAPILSTLPETTVV 149

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

- Database : SPTREMBL 25:*
- 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phage:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_virus:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*
 - 15: sp_virus:*
 - 16: sp_bacteriap:*
 - 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	793	100.0	176	12 Q9QRQ5	Q9QRQ5 hepatitis b
2	793	100.0	205	12 Q9QRQ6	Q9QRQ6 hepatitis b
3	793	100.0	212	12 Q91707	Q91707 hepatitis b
4	793	100.0	212	12 O11884	O11884 hepatitis b
5	793	100.0	212	12 Q89656	Q89656 hepatitis b
6	791	99.7	164	12 Q67904	Q67904 hepatitis b
7	790	99.6	183	12 Q8VBP8	Q8VBP8 hepatitis b
8	790	99.6	183	12 Q89437	Q89437 hepatitis b
9	790	99.6	183	12 Q88008	Q88008 hepatitis b
10	790	99.6	183	12 Q80582	Q80582 hepatitis b
11	790	99.6	212	12 Q91705	Q91705 hepatitis b
12	790	99.6	212	12 Q67876	Q67876 hepatitis b
13	790	99.6	212	12 Q68020	Q68020 hepatitis b
14	790	99.6	212	12 Q68012	Q68012 hepatitis b
15	790	99.6	212	12 Q89597	Q89597 hepatitis b
16	788	99.4	212	12 Q68025	Q68025 hepatitis b

17	788	99.4	212	12 Q68068	Q68068 hepatitis b
18	788	99.4	212	12 Q68075	Q68075 hepatitis b
19	787	99.2	183	12 Q68066	Q68066 hepatitis b
20	787	99.2	212	12 Q68070	Q68070 hepatitis b
21	787	99.2	212	12 Q67984	Q67984 hepatitis b
22	787	99.2	212	12 Q91702	Q91702 hepatitis b
23	787	99.2	212	12 Q68032	Q68032 hepatitis b
24	787	99.2	212	12 Q80SD7	Q80SD7 hepatitis b
25	786	99.1	183	12 Q67989	Q67989 hepatitis b
26	786	99.1	212	12 Q91704	Q91704 hepatitis b
27	785	99.0	183	12 Q89531	Q89531 hepatitis b
28	785	99.0	212	12 Q91SV7	Q91SV7 hepatitis b
29	785	99.0	212	12 Q91SV6	Q91SV6 hepatitis b
30	785	99.0	212	12 Q91SV5	Q91SV5 hepatitis b
31	785	99.0	212	12 Q91SV4	Q91SV4 hepatitis b
32	785	99.0	212	12 Q91SV3	Q91SV3 hepatitis b
33	785	99.0	212	12 Q91SV2	Q91SV2 hepatitis b
34	785	99.0	212	12 Q91SV1	Q91SV1 hepatitis b
35	785	99.0	212	12 Q91SV0	Q91SV0 hepatitis b
36	785	99.0	212	12 Q91SV0	Q91SV0 hepatitis b
37	785	99.0	212	12 Q91SV0	Q91SV0 hepatitis b
38	785	99.0	212	12 Q91SV0	Q91SV0 hepatitis b
39	784	98.9	183	12 Q91SV0	Q91SV0 hepatitis b
40	784	98.9	183	12 Q8VBP6	Q8VBP6 hepatitis b
41	784	98.9	183	12 Q68048	Q68048 hepatitis b
42	784	98.9	212	12 Q67872	Q67872 hepatitis b
43	784	98.9	212	12 Q67912	Q67912 hepatitis b
44	784	98.9	212	12 Q68051	Q68051 hepatitis b
45	784	98.9	214	12 Q91T08	Q91T08 hepatitis b

ALIGNMENTS

RESULT 1

Q9QRQ5 PRELIMINARY; PRT; 176 AA.
ID C9QRQ5
AC C9QRQ5;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-OCT-2002 (TREMELrel. 22, Last annotation update)
DE Core protein (Fragment).
GN C.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mut 50;
RA Saxena A., Acharya S.K., Nayak B., Panda S.K.;
RT "HBV mutants in non-A to E acute liver failure patients in India."
RL Submitted (DEC-1998) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AFL15425; AAD49194.1; -
DR InterPro; IPR002006; Hepatitis core.
DR Pfam; PF00306; Hepatitis_core; 1.
DR NON_TER 176
SQ SEQUENCE 176 AA; 20297 MW; 28397ABF657D93F4 CRC64;

Query Match 100.0%; Score 793; DB 12; Length 176;
Best Local Similarity 100.0%; Pred. No. 1.5e-80;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDIDPYKEFGATVELLSFLPSPFFSVRLDITASALYREALESPHCSPHETALRQAIL 60
Db 1 MDIDPYKEFGATVELLSFLPSPFFSVRLDITASALYREALESPHCSPHETALRQAIL 60
QY 61 CWGELMTLWTWGVNLEDPASRDLVVSYVNTNMGKFRQLLWFWHISCLTFGRETVEYLV 120
Db 61 CWGELMTLWTWGVNLEDPASRDLVVSYVNTNMGKFRQLLWFWHISCLTFGRETVEYLV 120
QY 121 SFGWIRTPPAYRPPNAPILSTLPETTVV 149
Db 121 SFGWIRTPPAYRPPNAPILSTLPETTVV 149

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RESULT 2
Q90R06 PRELIMINARY; PRT; 205 AA.
AC Q90R06;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Precore/core protein (Fragment).
GN C.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mut 50;
RA Saxena A., Acharya S.K., Nayak B., Panda S.K.;
RT "HBV mutants in non-A to E acute liver failure patients in India.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF115425; AAD49193.1; -.
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
FT NON_TER 205
SQ SEQUENCE 205 AA; 23531 MW; ASCF2117AC9938E6 CRC64;

Query Match 100.0%; Score 793; DB 12; Length 205;
Best Local Similarity 100.0%; Pred. No. 1.9e-80;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 60
Db 30 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 89

QY 61 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGKFKROLLWFWHISCLTFFGRETVEIYL 120
Db 90 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGKFKROLLWFWHISCLTFFGRETVEIYL 149

QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTV 149
Db 150 SFGVWIRTPPAYRPPNAPILSTLPETTV 178

RESULT 3
Q91J77 PRELIMINARY; PRT; 212 AA.
AC Q91J77;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Pre-core protein.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=119-Fam E;
RA Zampino R., Lobello S., Chiaramonte M., Venturi-Pasini C., Dumpis U.,
RT "Intra-familial transmission of Hepatitis B virus in Italy;
RT Phylogenetic sequence analysis and amino acid variation of the core
RT Gene.";
RL J. Hepatol. 0:0-0(2002).
DR EMBL; AF419515; AAL15943.1; -.
DR PIR; S33686; S33686.
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
FT CHAIN 30 212 CORE PROTEIN.
SQ SEQUENCE 212 AA; 24377 MW; B9C16A527905AF8 CRC64;

Query Match 100.0%; Score 793; DB 12; Length 212;
Best Local Similarity 100.0%; Pred. No. 1.9e-80;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 60
Db 30 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 89

QY 61 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGKFKROLLWFWHISCLTFFGRETVEIYL 120
Db 90 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGKFKROLLWFWHISCLTFFGRETVEIYL 149

QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTV 149
Db 150 SFGVWIRTPPAYRPPNAPILSTLPETTV 178

RESULT 4
O11884 PRELIMINARY; PRT; 212 AA.
AC O11884;
DT 01-JUL-1997 (TReMBLrel. 04, Created)
DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Core antigen (Core and e antigens).
GN C.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CH2-OHF;
RA Duong T.N., Michitaka K., Chen Y., Horike N., Kawai K., Onji M.;
RT "A comparison of genotype C and D hepatitis B virus: a clinical and
RT molecular biological study.";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBSJ databases.
DR EMBL; U95551; AAB59971.1; -.
DR PIR; C94409; NKVLA3.
DR PIR; S33686; S33686.
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
SQ SEQUENCE 212 AA; 24360 MW; D301689E8B05A1B8 CRC64;

Query Match 100.0%; Score 793; DB 12; Length 212;
Best Local Similarity 100.0%; Pred. No. 1.9e-80;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 60
Db 30 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 89

QY 61 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGKFKROLLWFWHISCLTFFGRETVEIYL 120
Db 90 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGKFKROLLWFWHISCLTFFGRETVEIYL 149

QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTV 149
Db 150 SFGVWIRTPPAYRPPNAPILSTLPETTV 178

RESULT 5
Q89656 PRELIMINARY; PRT; 212 AA.
AC Q89656;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Core antigen (Precore protein) (Core and e antigen).
GN PREC OR C.

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"HBV core sequence: definition of genotype-specific variability and correlation with geographic origin."
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF324140; AAL31853.1; -;
 DR InterPro; IPR002006; Hepatitis core.
 DR Pfam; PF00906; Hepatitis core; 1.
 DR SEQUENCE 183 AA; 21100 MW; 62D9CA5700042559 CRC64;

Query Match 99.6%; Score 790; DB 12; Length 183;
 Best Local Similarity 99.3%; Pred. No. 3.4e-80;
 Matches 148; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRAIL 60
 DB 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRAIL 60
 QY 61 CWGELMTLATWGVNLEDPASRDLVVSYNTNMGKFRQLLWFIHISCLTFGRETVEIYLV 120
 DB 61 CWGELMTLATWGVNLEDPASRDLVVSYNTNMGKFRQLLWFIHISCLTFGRETVEIYLV 120
 QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVV 149
 DB 121 SFGVWIRTPPAYRPPNAPILSTLPETTVV 149

RESULT 8

Q89437 PRELIMINARY; PRT; 183 AA.
 AC Q89437;
 DT 01-NOV-1996 (TREMELrel. 01, Created)
 DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
 DT 01-OCT-2002 (TREMELrel. 22, Last annotation update)
 DE Core protein (X, PREC and C genes) (CASTAA 2).
 GN CORE.
 OS Hepatitis B virus, and
 OS Hepatitis B virus (subtype ayw).
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407; 10418;
 RN [1]
 RP SEQUENCE FROM N.A.
 RQ SPECIES=Hepatitis B virus; STRAIN=I59;
 RA Jazayeri M., Sran N., Gish R., Basuni A.A., Cooksley G., Locarnini S.,
 RA Carman W.F.;
 RT "HBV core sequence: definition of genotype-specific variability and
 correlation with geographic origin."
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RQ SPECIES=Hepatitis B virus (subtype ayw);
 RA Lai M.E., Mazzoleni A.P., Porru A., Balestrieri A.;
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RQ SPECIES=Hepatitis B virus (subtype ayw);
 RA Karayiannis P.;
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RQ SPECIES=Hepatitis B virus (subtype ayw);
 RA Karayiannis P.;
 RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF324146; AAL31859.1; -;
 DR EMBL; X85289; CAAS2607.1; -;
 DR EMBL; X80925; CAAS6888.1; -;
 DR InterPro; IPR002006; Hepatitis core.
 DR Pfam; PF00906; Hepatitis core; 1.
 DR SEQUENCE 183 AA; 21102 MW; 2B9902063F253228 CRC64;

Query Match 99.6%; Score 790; DB 12; Length 183;
 Best Local Similarity 99.3%; Pred. No. 3.4e-80;
 Matches 148; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRAIL 60
 DB 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRAIL 60
 QY 61 CWGELMTLATWGVNLEDPASRDLVVSYNTNMGKFRQLLWFIHISCLTFGRETVEIYLV 120
 DB 61 CWGELMTLATWGVNLEDPASRDLVVSYNTNMGKFRQLLWFIHISCLTFGRETVEIYLV 120
 QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVV 149
 DB 121 SFGVWIRTPPAYRPPNAPILSTLPETTVV 149

Query Match 99.6%; Score 790; DB 12; Length 183;
 Best Local Similarity 99.3%; Pred. No. 3.4e-80;
 Matches 148; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRAIL 60
 DB 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRAIL 60
 QY 61 CWGELMTLATWGVNLEDPASRDLVVSYNTNMGKFRQLLWFIHISCLTFGRETVEIYLV 120
 DB 61 CWGELMTLATWGVNLEDPASRDLVVSYNTNMGKFRQLLWFIHISCLTFGRETVEIYLV 120
 QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVV 149
 DB 121 SFGVWIRTPPAYRPPNAPILSTLPETTVV 149

DB 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRAIL 60
 QY 61 CWGELMTLATWGVNLEDPASRDLVVSYNTNMGKFRQLLWFIHISCLTFGRETVEIYLV 120
 DB 61 CWGELMTLATWGVNLEDPASRDLVVSYNTNMGKFRQLLWFIHISCLTFGRETVEIYLV 120
 QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVV 149
 DB 121 SFGVWIRTPPAYRPPNAPILSTLPETTVV 149

RESULT 9

Q68008 PRELIMINARY; PRT; 183 AA.
 AC Q68008;
 DT 01-NOV-1996 (TREMELrel. 01, Created)
 DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
 DT 01-OCT-2002 (TREMELrel. 22, Last annotation update)
 DE Core protein.
 GN CORE.
 OS Hepatitis B virus.
 OS Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RQ SPECIES=Hepatitis B virus; STRAIN=I59;
 RA Lai M.E., Mazzoleni A.P., Porru A., Balestrieri A.;
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X85284; CAAS59596.1; -;
 DR InterPro; IPR002006; Hepatitis core.
 DR Pfam; PF00906; Hepatitis core; 1.
 DR SEQUENCE 183 AA; 21102 MW; 50BD9763F25E958 CRC64;

Query Match 99.6%; Score 790; DB 12; Length 183;
 Best Local Similarity 99.3%; Pred. No. 3.4e-80;
 Matches 148; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRAIL 60
 DB 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRAIL 60
 QY 61 CWGELMTLATWGVNLEDPASRDLVVSYNTNMGKFRQLLWFIHISCLTFGRETVEIYLV 120
 DB 61 CWGELMTLATWGVNLEDPASRDLVVSYNTNMGKFRQLLWFIHISCLTFGRETVEIYLV 120
 QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVV 149
 DB 121 SFGVWIRTPPAYRPPNAPILSTLPETTVV 149

RESULT 10

Q805R2 PRELIMINARY; PRT; 183 AA.
 AC Q805R2;
 DT 01-JUN-2003 (TREMELrel. 24, Created)
 DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
 DE Core protein.
 GN CORE.
 OS Hepatitis B virus.
 OS Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RQ SPECIES=Hepatitis B virus; STRAIN=I59;
 RA Chen Y., Michitaka K., Matsubara H., Yamamoto K., Horike N., Onji M.;
 RA "Complete genome sequence of hepatitis B virus (HBV) from a patient
 with fulminant hepatitis without precore and core promoter mutations:
 comparison with HBV from a patient with acute hepatitis infected from
 the same infectious source."
 RT J. Hepatol. 38:84-90 (2003).
 RL EMBL; AB078031; BACS4833.1; -;
 DR EMBL; AB078032; BACS4836.1; -;

QY 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRAIL 60
 DB 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRAIL 60
 QY 61 CWGELMTLATWGVNLEDPASRDLVVSYNTNMGKFRQLLWFIHISCLTFGRETVEIYLV 120
 DB 61 CWGELMTLATWGVNLEDPASRDLVVSYNTNMGKFRQLLWFIHISCLTFGRETVEIYLV 120
 QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVV 149
 DB 121 SFGVWIRTPPAYRPPNAPILSTLPETTVV 149

RESULT 10

Q805R2 PRELIMINARY; PRT; 183 AA.
 AC Q805R2;
 DT 01-JUN-2003 (TREMELrel. 24, Created)
 DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
 DE Core protein.
 GN CORE.
 OS Hepatitis B virus.
 OS Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RQ SPECIES=Hepatitis B virus; STRAIN=I59;
 RA Chen Y., Michitaka K., Matsubara H., Yamamoto K., Horike N., Onji M.;
 RA "Complete genome sequence of hepatitis B virus (HBV) from a patient
 with fulminant hepatitis without precore and core promoter mutations:
 comparison with HBV from a patient with acute hepatitis infected from
 the same infectious source."
 RT J. Hepatol. 38:84-90 (2003).
 RL EMBL; AB078031; BACS4833.1; -;
 DR EMBL; AB078032; BACS4836.1; -;

QY 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRAIL 60
 DB 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRAIL 60
 QY 61 CWGELMTLATWGVNLEDPASRDLVVSYNTNMGKFRQLLWFIHISCLTFGRETVEIYLV 120
 DB 61 CWGELMTLATWGVNLEDPASRDLVVSYNTNMGKFRQLLWFIHISCLTFGRETVEIYLV 120
 QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVV 149
 DB 121 SFGVWIRTPPAYRPPNAPILSTLPETTVV 149

QY 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRAIL 60
 DB 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRAIL 60
 QY 61 CWGELMTLATWGVNLEDPASRDLVVSYNTNMGKFRQLLWFIHISCLTFGRETVEIYLV 120
 DB 61 CWGELMTLATWGVNLEDPASRDLVVSYNTNMGKFRQLLWFIHISCLTFGRETVEIYLV 120
 QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVV 149
 DB 121 SFGVWIRTPPAYRPPNAPILSTLPETTVV 149

QY 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRAIL 60
 DB 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRAIL 60
 QY 61 CWGELMTLATWGVNLEDPASRDLVVSYNTNMGKFRQLLWFIHISCLTFGRETVEIYLV 120
 DB 61 CWGELMTLATWGVNLEDPASRDLVVSYNTNMGKFRQLLWFIHISCLTFGRETVEIYLV 120
 QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVV 149
 DB 121 SFGVWIRTPPAYRPPNAPILSTLPETTVV 149

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DR EMBL; AB078033; BAC54839.1; -.
DR InterPro; IPR002006; Hepatitis core.
DR Pfam; PF00906; Hepatitis core; 1.
SQ SEQUENCE 183 AA; 21130 MW; 1B39CDC97BDA0319 CRC64;

Query Match          99.6%; Score 790; DB 12; Length 183;
Best Local Similarity 99.3%; Pred. No. 3.4e-80;
Matches 148; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
DB 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60

QY 61 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGLKFRQLLWFHISCLTFGRETVEIYLV 120
DB 61 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGLKFRQLLWFHISCLTFGRETVEIYLV 120

QY 121 SFGWIRTPPAYRPPNAPILSTLPETTVV 149
DB 121 SFGWIRTPPAYRPPNAPILSTLPETTVV 149

RESULT 11
Q917J5 PRELIMINARY; PRT; 212 AA.
ID Q917J5
AC Q917J5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Pre-core protein.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=I21-Fam E;
RA Zampino R., Lobello S., Chiaramonte M., Venturi-Pasini C., Dumpis U.,
RA Thurez M., Karayiannis P.;
RT "Intra-familial transmission of Hepatitis B virus in Italy;
RT Phylogenetic sequence analysis and amino acid variation of the core
gene.";
RL J. Hepatol. 0:0-0(2002).
DR EMBL; AF419517; AAL15945.1; -.
DR PIR; S33686; S33686.
DR InterPro; IPR002006; Hepatitis core.
DR Pfam; PF00906; Hepatitis core; 1.
FT CHAIN 30 212 CORE PROTEIN.
SQ SEQUENCE 212 AA; 24412 MW; 19D58A4E8B05B243 CRC64;

Query Match          99.6%; Score 790; DB 12; Length 212;
Best Local Similarity 99.3%; Pred. No. 4.1e-80;
Matches 148; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
DB 30 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 89

QY 61 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGLKFRQLLWFHISCLTFGRETVEIYLV 120
DB 90 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGLKFRQLLWFHISCLTFGRETVEIYLV 149

RESULT 12
Q67876 PRELIMINARY; PRT; 212 AA.
ID Q67876
AC Q67876;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

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DE Pre C/C ORF.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RA Lai M.E., Mazzoleni A.P., Balestrieri A., Melis A., Portu A.;
RT "Sequence analysis of HBV genomes isolated from patients with HBsAg
RT negative chronic liver disease.";
RL Submitted (MAR-1992) to the EMBL/GenBank/DBJ databases.
DR EMBL; X65258; CAA46354.1; -.
DR PIR; C94409; NKVLA3.
DR PIR; S20750; S20750.
DR PIR; S33686; S33686.
DR InterPro; IPR002006; Hepatitis core.
DR Pfam; PF00906; Hepatitis core; 1.
SQ SEQUENCE 212 AA; 24348 MW; 6E91CC7D068EB573 CRC64;

Query Match          99.6%; Score 790; DB 12; Length 212;
Best Local Similarity 99.3%; Pred. No. 4.1e-80;
Matches 148; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
DB 30 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 89

QY 61 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGLKFRQLLWFHISCLTFGRETVEIYLV 120
DB 90 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGLKFRQLLWFHISCLTFGRETVEIYLV 149

QY 121 SFGWIRTPPAYRPPNAPILSTLPETTVV 149
DB 150 AFGWIRTPPAYRPPNAPILSTLPETTVV 178

RESULT 13
Q68020 PRELIMINARY; PRT; 212 AA.
ID Q68020
AC Q68020;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Pre-c/core protein.
GN PRE-C/CORE.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RA Lai M.E., Mazzoleni A.P., Portu A., Balestrieri A.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; X85291; CAA59611.1; -.
DR PIR; C94409; NKVLA3.
DR PIR; S33686; S33686.
DR PIR; S53211; S53211.
DR InterPro; IPR002006; Hepatitis core.
DR Pfam; PF00906; Hepatitis core; 1.
SQ SEQUENCE 212 AA; 24336 MW; 63006A4E8B04A1B8 CRC64;

Query Match          99.6%; Score 790; DB 12; Length 212;
Best Local Similarity 99.3%; Pred. No. 4.1e-80;
Matches 148; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
DB 30 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 89

QY 61 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGLKFRQLLWFHISCLTFGRETVEIYLV 120
DB 90 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGLKFRQLLWFHISCLTFGRETVEIYLV 149

QY 121 SFGWIRTPPAYRPPNAPILSTLPETTVV 149

```

Db 150 SFGWIRTPPAYRPPNAPILSTLPETTV 178

RESULT 14

Q68012 PRELIMINARY; PRT; 212 AA.

AC Q68012

DT 01-NOV-1996 (TREMELrel. 01, Created)

DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)

DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)

DE Pre-C/core protein.

GN Hepatitis B virus.

OS Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.

OC NCBI_TaxID=10407;

OX [1]

RN SEQUENCE FROM N.A.

RA Lai M.E., Mazzoleni A.P., Porru A., Balestrieri A.

RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.

DR EMBL; X85286; CAA59600.1; -

DR PIR; S33686; S33686.

DR PIR; S53200; S53200.

DR InterPro; IPR002006; Hepatitis core.

DR Pfam; PF00906; Hepatitis core; 1.

DR SEQUENCE 212 AA; 24250 MW; D30179D05DCD51B8 CRC64;

Query Match 99.6%; Score 790; DB 12; Length 212;

Best Local Similarity 99.3%; Pred. NO. 4.1e-80;

Matches 148; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHTALRQAIL 60

Db 30 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHTALRQAIL 89

QY 61 CWGELMTLATWGVNLEDPASRDLVVSYVNTNMGLKFRQLLWFHISCLTFGRETVEYLV 120

DL 90 CWGELMTLATWGVNLEDPASRDLVVSYVNTNMGLKFRQLLWFHISCLTFGRETVEYLV 149

QY 121 SFGWIRTPPAYRPPNAPILSTLPETTV 149

DL 150 SFGWIRTPPAYRPPNAPILSTLPETTV 178

RESULT 15

Q89597 PRELIMINARY; PRT; 212 AA.

AC Q89597

DT 01-NOV-1996 (TREMELrel. 01, Created)

DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)

DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)

DE HECAG (PRE-CORE protein) (PRECORE/core protein).

OS Hepatitis B virus (subtype ayw), and

OS Hepatitis B virus.

OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.

OC NCBI_TaxID=10418, 10407;

RN [1]

RN SEQUENCE FROM N.A.

RC SPECIES=Hepatitis B virus (subtype ayw); STRAIN=SUB-TYPE AYW;

RX MEDLINE=94079539; PubMed=8257295;

RA Preisler-Adams S., Schlayer M.J., Peters T., Hettler F., Gerok W.,

RA Rasenack J.

RT "Sequence analysis of hepatitis B virus DNA in immunologically

RT negative infection."

RL Arch. Virol. 133:385-396(1993).

RN [2]

RN SEQUENCE FROM N.A.

RC SPECIES=Hepatitis B virus (subtype ayw); STRAIN=AYW;

RA Karayiannis P.

RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.

RN [3]

RN SEQUENCE FROM N.A.

RC SPECIES=Hepatitis B virus (subtype ayw); STRAIN=AYW;

RA Karayiannis P.

Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.

(4)

RN SEQUENCE FROM N.A.

RP SPECIES=Hepatitis B virus; STRAIN=I43-Fam G;

RC Zampino R., Lobello S., Chiaramonte M., Venturi-Pasini C., Dumpis U.,

RA Thurez M., Karayiannis P.

RT "Intra-familial transmission of Hepatitis B virus in Italy:

RT Phylogenetic sequence analysis and amino acid variation of the core

RT gene."

RL J. Hepatol. 0:0-0(2002).

RN [5]

RN SEQUENCE FROM N.A.

RP SPECIES=Hepatitis B virus; STRAIN=Gaml119F29, and Gaml821F217;

RC Dumpis U., Mendy M., Karayiannis P.;

RA "Prevalence of HBV core promoter/precore/core mutations in Gambian

RT chronic carriers."

RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; X72702; CAA51257.1; -

DR EMBL; X80925; CAA56887.1; -

DR EMBL; AP419525; AAL15953.1; -

DR EMBL; AF350127; AAK57244.1; -

DR EMBL; AF350205; AAK57322.1; -

DR PIR; C94409; NKVLA3.

DR PIR; S32204; S32204.

DR PIR; S33686; S33686.

DR InterPro; IPR002006; Hepatitis core.

DR Pfam; PF00906; Hepatitis core; 1.

DR SEQUENCE 212 AA; 24336 MW; 1861B13E8B047AC8 CRC64;

FT CHAIN 30 212 CORE PROTEIN

SQ

Query Match 99.6%; Score 790; DB 12; Length 212;

Best Local Similarity 99.3%; Pred. NO. 4.1e-80;

Matches 148; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHTALRQAIL 60

Db 30 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHTALRQAIL 89

QY 61 CWGELMTLATWGVNLEDPASRDLVVSYVNTNMGLKFRQLLWFHISCLTFGRETVEYLV 120

Db 90 CWGELMTLATWGVNLEDPASRDLVVSYVNTNMGLKFRQLLWFHISCLTFGRETVEYLV 149

QY 121 SFGWIRTPPAYRPPNAPILSTLPETTV 149

Db 150 SFGWIRTPPAYRPPNAPILSTLPETTV 178

Search completed: April 23, 2004, 16:29:38

Job time : 40 secs